Mon Aug 12 17:16:21 2002

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
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August 12, 2002, 17:19:43; Search time 27.08 Seconds (without alignments) 28.387 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 1 gywgkgyw 8 10-071247-1 59 Title: Perfect score: Sequence: Scoring table: Run on:

Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	res	short-chain fatty	hypothetical prote			_				acetyltransferase	conserved hypothet	probable formylmet	mannosyl-glycoprot	beta-N-acetylhexos	beta-N-acetylhexos	Ig heavy chain V r	transposase - Dein	hypothetical prote	DNA ligase (ATP) (	UDPglucoseglycop	hypothetical prote	hypothetical prote	saposin precursor	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	hypothetical prote	
SUMMARIES	qi	BVBYK5	F83694	E69903	G83047	H83554	B72567	AC2394	D83812	A83915	AE2918	н97692	A69491	A56390	E95006	A97879	PH1663	F75337	A12041	137079	863669	S77357	AD1927	A28716	B29514	A29476	11	S47572	S73827	B72742
	DB	-	7	7	7	7	7	7	7	7	7	7	~	7	~	7	~	7	7	7	~	7	7	П	~	7	7	~	~	7
	Query Match Length	-	441	83	187	358	470	80	180	181	196	207	563	1311	1312	1312	113	145	375	844	1447	489	495	554	589	589	590	590	741	102
dР	Query	7.67	76.3	73.7	73.7	72.9	72.9	71.2	71.2	71.2	71.2	71.2	71.2	× 71.2	71.2	71.2	69.5	69.5	69.5	69.5	69.5	67.8	67.8	67.8	67.8	67.8	67.8	67.8	67.8	66.1
	Score	47	45	43.5	43.5	43	43	42	42	42	42	42	42		42	42	41	41	41	41	41	40	40	40	40	40	40	40	40	39
	Result No.	1	7	m	4	S	9	7	<b>6</b> 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

acetyltransferase, conserved hypothet	acetyltransferase,	hypothetical prote	hypothetical prote	secretory protein-	probable heme tran	probable phosphoes	hypothetical prote	hypothetical prote	INDA1 protein - fu	cyclomaltodextrin	probable membrane	G protein-coupled	probable ABC trans	protein F18014.29
D87288 B97933	A95066	H22845	826009	T47883	S70854	G83242	T04561	T36462	S33212	ALKBG	S67568	JC5808	E95268	B86328
00	7	7	7	~	Н	М	~	7	٦	Н	~	~	~	7
177	186	194	228	247	250	270	396	499	573	655	961	962	273	115
66.1 66.1	66.1	66.1	66.1	66.1	66.1	1.99	66.1	66.1	66.1	66.1	66.1	66.1	65.3	64.4
36 36	39	39	39	39	39	39	39	39	39	39	39	39	38.5	38

## ALIGNMENTS

	RESULT 1 BVBYK5
	killer toxin resistance protein KRE5 precursor – yeast (Saccharomyces cerevisiae) Nylternate names: protein O6254; protein YOR336w C:Species: Saccharomyces cerevisiae
	C;Deter: 30: Sep-1991 #sequence_revision 10-May-1996 #text_change 16-Jun-2000 C:Acression: 562066: A36327: S67243: S71974: S12202
	R; Parle, A.G.; Hand, N.J.; Goulding, S.G.; Wolfe, K.H. submitted to the EMBL Data Library, June 1995
	A; Description: Sequence of 29 kilobases around the PDR10 locus on the right arm of Sa A; Reference number: S62058
	A; Accession: \$62066 A; Molecule type: DNA
	A; Residues: 1-1365 <par> A; Cross-references: EMBL: 249821; NID: 91163062; PIDN: CAA89981.1; PID: 91163070</par>
_	R;Meaden, P.; Hill, K.; Wagner, J.; Slipetz, D.; Sommer, S.S.; Bussey, H. Mol. Cell, Biol. 10, 3013-3019, 1990
	A; Title: The yeast KRE5 gene encodes a probable endoplasmic reticulum protein require
	A; Accession: A36327
_	A) MODECULE type: DNA *** DAG
_	A. A. C.
	R; Goulding, S.E.; Hand, N.J.; Parle-McDermott, A.G.; Wolfe, K.H.
	Bunilted to the Frotein Sequence Database, July 1990 B.Reference number: 667233
	A.A. Accession: 567243
	A;Molecule type: DNA
	%/COSS-TEST   STATE
	A. Experimental source: strain S288C
	R:Parle-McDermott, A.G.; Hand, N.J.; Goulding, S.E.; Wolfe, K.H. yeast 12. 999-1004. 1996
	Autitie: Sequence of 29 kb around the PDR10 locus on the right arm of Saccharomyces c
	A;Reference number: S71966; MUID:97051586 A:Accesion: G71974
	A; Status: nucleic acid sequence not shown; translation not shown
	A;Molecule type: DNA A:Residues: 1-1365 <paw></paw>
	PID:91163070
	A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
	Cygenel.ccs; MIPS:YOR336w
	A;Cross-references: SGD:S0005863; MIPS:YOR336w
	A;Map position: 15R C:Runction:
	A Description: required for normal cell growth
	A;ratnway: (1->0)-beta-b-glucan blosyntnesis C;Superfamily: KRE5 protein
	C, Keywords: endoplasmic reticulum; glycoprotein
	F:14-17/Domain: signal sequence #status predicted <5167. F:18-136/Product: killer toxin resistance orotein KRE5 #status predicted <mat></mat>
	and property of the second

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Query Match
Best Local Similarity
Matches 6; Conserv
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A; Molecule type: DNA
A; Residues: 1-187 <STO>
                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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hypothetical protein yod! - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: E6903
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D; Emmerson, P.T.; Entian, K.D.; Errington, J.; Parero, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Evinita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Evinita, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portoria,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sakiguchi, J.; Sckowska, A.; Sconlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sakiguchi, J.; Sckowska, A.; Serol
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Titte: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accerican
                                                                                                                                                                                                                                                                                                                                                                                                           Species: Bacilius halodurans
C;Species: Bacilius halodurans
C;Date: Ol-Dec-2000 #sequence_revision Ol-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83694
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G;; Sasaki, R; Masui, N; Fuji, F; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04077.1; GSPDB:GN0d
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:299114; GB:AL009126; NID:92634230; PIDN:CAB13852.1; PID:e1185432;
A;Experimental source: strain 168
                          U
F:1362-1365/Region: endoplasmic reticulum retention signal #status predicted F:115,228,293,457,519,523,604,644,870,1091,1150,1195/Binding site: carbohydrate (Asn)
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-83 <KGN>
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                                                                                                                                                                         Gaps
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C;Superfamily: conserved hypothetical integral membrane protein HP0693
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                                                                                                              Score 47; DB 1;
Pred. No. 31;
1; Mismatches
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Pred. No. 22;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                              Query Match 79.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-441 <STO>
                                                                                                                                                                                                                                                                                    Db 1234 GYWKEGYW 1241
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A;Gene: yodI
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hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)
c) species: Pseudomonas aeruginosa
c) species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: H83554
R; Stover, C.K.; Phan, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; R; Stover, C.K.; Ptan, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Lory, S.; Olson, M.V.
Nature 406, 955-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID: 20437337
A; Status: preliminary
A; Reference number: ASPERTOS
                                                                                                                                                                                                                                                                                                                                            Cipecies: Pseudomonas aeruginosa
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
CiAccession: G83047
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.;
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004892; GB:AE004091; NID:99951049; PIDN:AAG08179.1; GSPDB:GN A;Rxperimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA0736
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hypothetical protein PA4793 [imported] - Pseudomonas aeruginosa (strain PAO1)
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87.5%; Pred. No. 17;
iive 0; Mismatches 0;
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0
   DB 2;
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Score 43.5; DB Pred. No. 8.5; 0; Mismatches
   73.7%;
87.5%;
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                                                             Conservative
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Gaps

; 0

Length 180;

5

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hypothetical protein BH2121 [imported] - Bacillus halodurans (strain C-125)
(Specias: Bacillus halodurans
C;Specias: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83915
C;Accession: A83915
C;Accession: A83915
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83915
A;Accession: A83915
A;Accession: A83915
A;Residues: 1-181 <STO>
A;Coss-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05840.1; GSPDB:CAA;Genetics: BH2121
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 11-3an-2002
C;Accession: AE5918
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, X.; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, X.; Wooderage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Sesiduse: 1-180 (STO>
A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05019.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1300
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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A; Morecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB: AEON08688; PIDN: AAL43763.1; PID: 917741299; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Genetics:
A; Genetics:
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28;
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28;
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                                                                                                                                                                                                                                                                                                                                                                                                          71.2%; Score 42; DB 100.0%; Pred. No. 28; ive 0; Mismatches
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                             hypothetical protein APE1820 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum perni
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NA Res. 8, 205-213, 2001

NA Fatile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; WUID:2159285; PMID:11759840

A; Accession: AC2394

A; Accession: AC2394

A; Molecule type: DNA

A
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C; Species: Bacillus halodurans
C; Species: Dacillus halodurans
C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C; Accession: DB3812
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: D83812
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A.Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C.Acceston: 44-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
R.Kaneko, T.; Nakamura
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46;
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Pred. No. 46;
1; Mismatches
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Pred. No. 13;
0; Mismatches
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.9%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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329 WGRGYW 334
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C;Species: Streptococcus pneumoniae
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C;Accession: A56390
A;Title: Cloning and expression of the beta-N-acetylglucosaminidase gene from Strepto A;Title: Cloning and expression of the beta-N-acetylglucosaminidase gene from Strepto A; Reference number: A56390; MUID:95238375
A;Reference number: A56390
A;Status: preliminary
A;Residues: 1-1311 <CLA>
A;Cross-references: GB:L36923; NID:g784896; PIDN:AAC41450.1; PID:g784897
C;Genetics:
A;Gene: strH
C;Reywords: glycosidase; hydrolase; tandem repeat
F;1-33/Domain: signal sequence #status predicted <SIG>
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C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C; Accession: E95006
R; Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Residues: Pellininary
A; Residues: 1-1312 < KUR>
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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97879
C;Accession: A97872
C;Accession: A97872
C;Accession: A7872
C;Accession: A7872
A771416: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A786erence number: A97872; MUID: 21429245; PMID: 11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-N-acetylhexosaminidase [imported] - Streptococcus pneumoniae (strain TIGR4)
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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A56390
mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - Strept
                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession. H97692
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein BH0837 (AP001510) [imported] - Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum/tungsten) chain A C;Species: Archaeoglobus fulgidus
C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-207 KURN>
A, Cross-references: GB: AEO07869; PIDN: AAK88497.1; PID: 915158008; GSPDB: GN00169
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100.0%; Pred. No. 31;
iive 0; Mismatches
               Pred. No. 30;
                                                   Mismatches
                                               0;
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A;Map position: circular chromosome
       100.08;
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
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           Best Local Similarity
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511 YWGRTYW 517
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                                                                                                                                                                           116 YWGKGY 121
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A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-1312 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK98861.1; PID:g15457590; GSPDB:GN00174
C;Genetics:
A;Gene: strH
C;Keywords: glycosidase; hydrolase
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ö Gaps 0; Query Match 71.2%; Score 42; DB 2; Length 1312; Best Local Similarity 71.4%; Pred. No. 1.6e+02; Matches 5; Conservative 1; Mismatches 1; Indels

2 ywgkgyw 8 || || || :| |871 YWSKGWW 877 δý

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Search completed: August 12, 2002, 17:22:44 Job time: 181 sec

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Mon Aug 12 17:16:21 2002

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - pròtein search, using sw model

August 12, 2002, 17:21:48 ; Search time 13.51 Seconds (without alignments) 22.928 Million cell updates/sec Run on:

10-071247-1 59

Title:

1 gywgkgyw 8 **BLOSUM62** Perfect score: Scoring table: Sequence:

105224 seqs, 38719550 residues Searched:

Gapop 10.0 , Gapext 0.5

of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3 saccharo	P49610 streptococc	Q9f5n7 burkholderi	_	schizos	Ol3035 gallus gall	rattus	Q9erz3 mus musculu	m	4 pos		P75443 mycoplasma	P38453 marchantia			Q9j5c7 fowlpox vir	P20626 corynebacte									P71756 mycobacteri		~	94	6	8	9332 dros	P33622 mus musculu
SUMMARIES	ΠD	E5_Y	STRH_STRPN	NORM_BURVI	DNL4_HUMAN	UGGG_SCHPO	SAP_CHICK	SAP_RAT	ACM3_MOUSE	ACM3_RAT	ACM3_BOVIN	ACM3_PIG	YD35_MYCPN	YM05_MARPO	INA1_TRIHA	CDGT_KLEPN	V093_FOWPV	PLD_CORPS	NAH2_RABIT	NAH2_HUMAN	NAH2_RAT	BUTY_MOUSE	BUTY_BOVIN	BUTY_HUMAN	YD14_HAEIN	PLYD_ERWCA	HEMN_MYCTU	ATOE_HAEIN	PSBB_SYNY3	PSBB_SYNP7	17	Y537_SYNY3	UGGG_DROME	APC3_MOUSE
	DB	П	-	-	Н	-	-1	7	П	-	Н	Н	Н	-	-	П	Н	М	-	-	-	П	Н	Н	П	П	<b>,</b>	-	Н	Н	-	М	Н.	Н
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oje)	Query	6	71.2	69.5	69.5	69.5	67.8	67.8	8.79	67.8	67.8	67.8	67.8	66.1	66.1	66.1	64.4	64.4	64.4	64.4	64.4	63.6	63.6	63.6	62.7	$\sim$	62.7	ä	ď	ς.	2	ä	62.7	61.0
	Score	4	42	41	41	41	40	40	40	40	40	40	40	39	38	39	38	38	38	38	38	37.5	37.5	37.5	37	37	37	37	37	37	37	37	37	36
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Q45537 bacillus su P17989 fibrobacter P80011 rhizobium m P55620 rhizobium s Q44678 corynebacte P76460 escherichia P50430 rattus norv O78511 guillardia P15848 homo sapien Q912a3 gorilla gor P20309 homo sapien Q912a4 pan troglod
CTJB_BACSU GUB_FIBSU TA3_RHIME Y 4PO_RHISN PURK_CORAM ATOE_ECOLI ARSB_RAT ARSB_GUITH ARSB_GUITH ARSB_HUMAN ACM3_GORGO ACM3_HUMAN
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100 349 440 4413 4440 5990 5990 5990
61.0 61.0 61.0 61.0 61.0 61.0 61.0 61.0
QQQQQQQQQQQQQ MMMMMMMMMM
4 5 8 8 8 8 9 8 9 8 9 8 9 9 9 9 9 9 9 9 9

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                      SECTEBROE FROM N.A.
MEDLINE=90258892; PubMed=2188106;
Meaden P., Hill K., Wagner J., Slipetz D., Sommer S.S., Bussey H.;
Meaden P., Hill K., Pagner J., Slipetz D., Sommer S.S., Bussey H.;
Meaden P., Hill K., Pegner J., Slipetz D., Sommer S.S., Bussey H.;
Meaden P., Hill K., Pagner J., Bussey H.;
Meaden P., Manner J., Bussey H.;
Meaden P., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIANE-97051586; PubMed-8896263;
MEDIANE-97051586; PubMed-8896263;
Parler Mcdermott A.G., Hand N.J., Goulding S.G., Wolfe K.H.;
Sequence of 29 Kb around the PDR10 locus on the right arm of
Saccharomyces cerevisiae chromosome XV: similarity to part of
Chromosome I.";
Yeast 12:999-1004(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL GROWTH.
-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-1- SIMILARITY: SOME, TO D.MELANOGASTER UGGG.
                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-NUV-1997 (Rel. 35, Last sequence update)
01-NUV-1997 (Rel. 35, Last annotation update)
11-NUV-1997 (Rel. 35, Last annotation update)
KRES OR YOR336W.
                                                            PRT; 1365 AA.
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                         KRE5_YEAST
P22023; Q12190;
01-AUG-1991 (Re]
KESULT 1
KRE5_YEAST
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                          EMBL;
TIGR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heldelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Purkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Pull I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATC 12213.
STRAIN=ATC 12213.
CONTINE—59238375; PubMed=7721787;
Clarke V.A., Platt N., Butters T.D.;
"Cloning and expression of the beta-N-acetylglucosaminidase gene from Streptococcus pneumoniae. Generation of truncated enzymes with modified aglycon specificity.";
                                                                                         MISSING (IN REF. 1).
HLDQNEVPETEHFEA -> ILIKMKCQKQNISKAK (IN
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 293:498-506(2001).
-!-CATALTYIC ACTIVITY: Hydrolysis of terminal non-reducing N-cataLTTIC ACTIVITY: Hydrolysis of terminal non-reducing N-cetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
-!-SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
-!-SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
-!-SIMILARITY: BELONGS TO FAMILY 20 OF GLYCOSYL HYDROLASES.
                           (POTENTIAL).
                                      (POTENTIAL)
                                                                (POTENTIAL)
                                                                                                                                                                                           .
0
              (POTENTIAL)
                                                                                                                                                               Score 47; DB 1; Length 1365; Pred. No. 7.1; 1; Mismatches 1; Indels
                                                                                                                             DOF5851175CC0333 CRC64;
                                                               N-LINKED (GLCNAC. . .) (POT PREVENT SECRETION FROM ER. MISSING (IN REF. 1).
N-LINKED (GLCNAC. .) ()
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N-LINKED (GLCNAC. .) (
                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Beta-N-acetylhexosaminidase precursor (EC 3.2.1.52).
                                                                                                                                                                                                                                                                                                        PRT; 1312 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 270:8805-8814(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=TIGR4;
MEDLINE=21357209; PubMed=11463916;
                                                                                                                              1365 AA; 156476 MW;
                                                                                                                                                                  79.7%;
75.0%;
                                                                                                                                                                  Query Match 79.7
Best Local Similarity 75.0
Matches 6; Conservative
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794
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                                                    CARBOHYD
CARBOHYD
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                             CARBOHYD
                                           CARBOHYD
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                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
CATALYTIC DOMAIN 1.
CATALYTIC DOMAIN 2.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fehlmer-Gardiner C.C., Valvano M.A.;
"Cloning and characterization of norm, encoding a multi-drug efflux protein from Burkholderia vietnamiensis.";
Submitted (OCT-2000) to the EMBL/Genbank/DDBJ databases.
-i- FUNCTION: FUNCTIONS AS A NA(+)/DRUG ANTIPORTER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
-!- SIMILARITY: BELONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE) FAMILY. NORM (TC 2.A.66.1.1) SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable multidrug resistance protein norM (Na(+)/drug antiporter)
                                                    InterPro; IPR001540; Glyco_hydro_20.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00728; Glyco_hydro_20; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Hydrolase; Glycosidase; Repeat; Transmembrane; Cell wall; Signal;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1; Length 1312;
Pred. No. 39;
                                                                                                                                                                                                                                  BETA-N-ACETYLHEXOSAMINIDASE.
EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503375B5257A90B5 CRC64;
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E (IN REF. 1).
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A (IN REF. 1).
R (IN REF. 1).
A (IN REF. 1).
A (IN REF. 1).
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1; Mismatches
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             AE007323; AAK74246.1; -. SP0057; -.
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burkholderia vietnamiensis.
EMBL; L36923; AAC41450.1;
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MEDIATE-95280920; PubMed-7760816;
MEDIATE-95280920; PubMed-7760816;
Well Y.-F., Robins P., Carter K., Caldecott K., Pappin D.J.C.,
Yu G.-L., Wang R.-P., Shell B.K., Nash R.A., Schar P., Barnes D.E.,
Haseltine W.A., Lindahl T.;
Molecular cloning and expression of human cDNAs encoding a novel DNA
ligase IV and DNA ligase III, an enzyme active in DNA repair and
Mol. Cell. Biol. 15:3206-3216(1995).
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel, 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase IV (EC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: TESTIS, THYMUS, PROSTATE AND HEART.
SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
SIMILARITY: CONTAINS 2 BRCT DOWAINS.
                                                                                                                                                                                                                                     4;
                                             Transport; Sodium transport; Transmembrane; Inner membrane.
TRANSMEM 56 76 POTENTIAL.
                                                                                                                                                                                                               Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + {decxyribonuclectide}(N) + {decxyribonuclectide}(M) = AMP + diphosphate + {decxyribonuclectide}(N+M).
                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                OCAFB2EC20652D11 CRC64;
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                  844 AA.
                                                                                                                                                                                                               Score 41; DB 3 Pred. No. 21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
send an email to license@isb-sib.ch).
                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                  POTENTIAL. POTENTIAL.
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InterPro; IPR000977; DNA_ligase.
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                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                MM;
                   EMBL; AF312031; AAG27731.1; -.
InterPro; IPR002528; UPF0013.
Pfam; PF01554; UPF0013; 2.
                                                                                                                                                                                                               69.5%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X83441; CAA58467.1; -.
                                                                                                                                                                                47860
                                                                                                                                                                                                              Query Match 69.5
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                  167
192
222
267
300
345
422
                                                                                                                                                                                                                                                                     408 GYWGIGFPTGYW 419
                                                                                                                                                                                                                                                        1 gywg----kgyw 8
                                                                                                                                                                              462 AA;
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1147
1172
202
2247
2280
3280
402
402
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P49917;
                                                                                 TRANSMEM
TRANSMEM
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PROSITE; PS50172; BRCT; 2.
PROSITE; PS50172; BRCT; 2.
PROSITE; PS0033; DNA_LIGASE_A1; 1.
PROSITE; PS00333; DNA_LIGASE_A3; 1.
PROSITE; PS50160; DNA_LIGASE_A3; 1.
DNA repair; DNA replication; DNA recombination; Cell division; Ligase; ATP-binding; Nuclear protein; Repeat.
DOMAIN 587 676
BRCT 1.
BROMAIN 741 844 BRCT 1.
BRNDING 206 206 AMP (BY SIMILARITY).
SEQUENCE 844 AA; 96154 MW; D48E16F211A3BE97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       absence of the enzyme from Saccharomyces cerevisiae.";
J. Biol. Chem. 269;30701-30706(1994)
-1- FUNCTION: UNFOLDED, DENATURED GLYCOPROTEINS ARE SUBSTANTIALLY
BETTER SUBSTRATES FOR GLUCOSYLATION BY THIS ENZYME THAN ARE THE
CORRESPONDING NATIVE PROFEINS. THIS PROTEIN AND TRANSIENT
GLUCOSYLATION MAY BE INVOLVED IN MONITORING AND/OR ASSISTING THE
FOLDING AND ASSENBLY OF NEMLY MADE GLYCOPROTEINS, IN ORDER TO
IDENTIFY GLXCOPROTEINS THAT NEED ASSISTANCE IN FOLDING FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fernandez F., Jannatipour M., Hellman U., Rokeach L.A., Parodi A.J.; "A new stress protein: synthesis of Schizosaccharomyces pombe UDP--GL:Glycoprotein glucosyltransferase mRNA is induced by stress conditions but the enzyme is not essential for cell viability."; EMBO J. 15:705-713(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
UDP-glucose:glycoprotein glucosyltansferase precursor (EC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SEQUENCE OF 19-31; 148-158; 401-412; 557-568; 723-730; 983-990 AND 1118-1130, FUNCTION, SUBCELLULAR LOCATION, CORACTOR, SUBUNIT, AND GLYCOSYLATION.
MEDLINE-96181349; Pubmed-8631292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95074086; PubMed-7982990;
Fernandez F.S., Trombetta S.E., Hellman U., Parodl A.J.;
"Purification to homogeneity of UDP-9lucose:glycoprotein
glucosyltransferase from Schizosaccharomyces pombe and apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: REQUIRES CALCIUM AND MANGANESE IONS FOR ACTIVITY.
-!- PATHWAY: GLYCOSYLATION.
-!- SUBUNIT: MONOMER.
-!- SUBCELLUTAR LOCATION: Endoplasmic reticulum lumen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.5%; Score 41; DB 1; Length 844; 100.0%; Pred. No. 37; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood V., Warren T., Harris D., Barrell B.G., Rajandream Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi, Ascomycota; Schizosaccharomycetels; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UDP-Glc:glycoprotein glucosyltransferase). GPT1 OR SPBPJ4664.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 19-31, AND CHARACTERIZATION.
Pfam; PF00533; BRCT; 2.
Pfam; PF01068; DNA_ligase; 1.
SMART; SM00292; BRCT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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SEQUENCE FROM N.A.
STRAIN=972;
Wood V., Warren T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altman N., Horowitz M.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: THE LYSSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A., AND SEQUENCE OF 194-203.
TISSUE-Brain, and Liver;
MEDLINE-99129745; PubMed-9461526;
Azuma N., Seo H.-C., Lie O., Fu Q., Gould R.M., Hiraiwa M., Burt D.W.
Paton I.R., Morrico D.R., O'Brien J.S., Kishimoto Y.;
"Cloning, expression and map assignment of chicken prosaposin.";
Biochem. J. 330:321-327(1998).
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proactivator polypeptide precursor [Contains: Saposin A; Saposin B; Saposin C; Saposin D].
                                                                                                                                                                                                        N-LINKED (GLCNAC...) (POTENTIAL).
T -> T (IN REF. 1).
T -> A (IN REF. 1).
T -> S (IN REF. 1).
T -> S (IN REF. 1).
T -> C (IN REF. 1).
T -> G (IN REF. 1).
T -> G (IN REF. 1).
                                                                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                    EMBL; AL591302; CAC38351.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Signal; Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1448;
                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                      UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 41;
                                                                                                                                                                                                                                                                                                                                                                         69.58;
                                                                                                             EMBL; U38417; AAB05993.1; -.
                                                                                                                                                                                                                                                                                                                                         165467
                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                            18
1448
                                                                                                                                                                                                                                                                                                                               1261
  -!- PTM: GLYCOSYLATED
                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus.
NCBI_TaxID=9031;
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                                                                                                                                                                  Glycoprotein.
SIGNAL
CHAIN 1
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013035;
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CONFLICT
CONFLICT
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CONFLICT
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SAP_CHICK
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THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).

CHOCTION: SABOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND GALACTOSYLCERAMIDE BY BETA-GLACOSYLCERAMIDASE (EC 3.2.1.46).

CHOSTIN C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC LIPPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING THE SUBSTRATE (BY SIMILARITY).

CHEBROSIDE SULFATE BY ARYLGULFATASE A (EC 3.1.6.8), GMI GANGLIOSIDES BY BETA-GLACTOSIDASE (EC 3.2.1.23) AND CLOBOTRIAOSYLCERAMIDE BY ALRUPAGALACTOSIDASE A (EC 3.2.1.22).

SAPOSIN-B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE SHINGOLIPID HYDROLASES (BY SIMILARITY).

CHOBOTRIAOSYLCERAMIDE BY ALRUPAGALACTOSIDASE A (EC 3.2.1.22).

SAPOSIN-B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE SHINGOLIPID HYDROLASES (BY SIMILARITY).

CHOSTIN SAPOSIN D IS A PRECIFIC SPHINGOMYELIN PHOSPHODIESTERASE ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).

CHOSTIN THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SWALL PEPTING HYDROLASE ACTIVATOR PROTEONS (BY SIMILARITY).

CHOSTIN THIS PRECURSOR IS PROTEONS (BY SIMILARITY).

CHOSTIN THIS PRECURSOR IS PROTEONS (BY SIMILARITY).

CHOSTIN THIS SHALL AND AND ARE SPHINGOLIPID PROTEOLYTICALLY PROCESSED TO 4 SWALL PETINGS (WHICH ARE SIMILARITY).

CHOSTIN THE STANDARINS SAPOSIN A TYPE DOMAINS.

CHOSTIN THE STANDARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SAPOSIN A.
SAPOSIN B.
SAPOSIN B.
SAPOSIN D.
SAPOSIN D.
SAPOSIN LIKE TYPE A 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 2.
BY SIMILARITY.
BY 
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SIGNAL 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> D (IN REF. 2).
B803000E891C3963
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InterPro; IPR003199; SapA.
InterPro; IPR003259; Saposin.
Pfam; PP02199; SAPA; 2.
ProDom; PD001732; SapB; 3.
ProDom; PD012221; Saposin; 1.
SMART; SM00162; SAPA; 2.
SMART; SM00118; SAPB; 4.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                        Gaps
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MDELINE=26175245, Pubmed=8601692;
MOTALES C.R., E1-Alfy M., Zhao Q., Igdoura S.A.;
"Expression and tissue distribution of rat sulfated glycoprotein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96128541; PubMed-8573994;
Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
Molecular rolle of sulfated glycoprotein-1 (SGP-1/prosaposin) in Serfoli cells.";
Histol. Histopathol. 10:1023-1034(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Sertoli cells,
MEDLINE-89000647; PubMed=3048385;
MEDLINE-89000647; PubMed=3048385;
MEDLINE-89000647; PubMed=3048385;
"Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat Sertoli cells: sequence similarity with the 70 kilodalton precursor to sulfatide/GMI activator.";
Biochemistry 27:4557-4564(1988).
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                         Score 40; DB 1; Length 518;
Pred. No. 33;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       SAP_RAT STANDARD; PRT; 554 AA. 10960; 062841; 064190; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 16-JUL-1980 (Rel. 40, Last annotation update) Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin). PSAP OR SGPI.
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InterPro; IPR003119; SapA.
InterPro; IPR003169; SapA.
InterPro; IPR003259; SapOsin.
Pfam; PF02199; SAPA.
Probom; PF01732; SapB; 3.
Probom; PF01732; SapB; 3.
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                            67.8%;
83.3%;
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SMART; SM00118; SAPB; 4.
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Query Match
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Thes 5; Conserve
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TISSUE-Brain;
MEDLINE-95179320; PubMed=7874308;
MEDLINE-95179320; PubMed=7874308;
Madre C., Dos Santos G., Koulakoff A.;
Tolitured neurons from mouse brain reproduce the muscarinic receptor profile of their tissue of origin.";
Eur. J. Neurosci. 6:1631-1701(1994).
-! FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENIAATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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                                           SAPOSIN-LIKE TYPE A 1.
SAPOSIN-LIKE TYPE A 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                  SULFATED GLYCOPROTEIN 1.
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09ERZ3; 064055;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Muscarinic accepylcholine receptor M3 (Mm3 mAChR).
CHRM3 OR CHRM-3.
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Pred. No. 3
Glycoprotein; Repeat.
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Best Local Similarity 83.30,
bear 5; Conservative
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SEQUENCE FROM N.A.
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Mammalia; Euthería; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Pfam, PROMOSI; TLL.1; 1.
PRINTS; PROMOSI; GPCRRINDESN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_CHANNEL; G_PROPROPENCEN; Transmembrane; Phostsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
FOR STRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                     SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-8726421; PubMed-3037705;
Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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Pred. No. 38;
0; Mismatches 2; Indels
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
           SUBCELLULAR LOCATION: Integral membrane protein
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01-AUG-1988 (Rel. 08, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CHRM3 OR CHRM-3.
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MGD; MGI:88398; Chrm3.
InterPro; IPR000276; GPCR_Rhodpsn.
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Best Local Similarity 71.4
Matches 5; Conservative
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Wess J., Maggio R., Palmer J.R., Vogel Z.;
Wess J., Maggio R., Palmer J.R., Vogel Z.;
Wess J., Maggio R., Palmer J.R., Vogel Z.;

binding and muscarinic receptor activation. A study with m3
muscarinic receptor point mutantes.;
J. Biol. Chem. 267:19313-19319(1992)
-|- FUNCTION: THE MUSCARINIC ACEPTICCHINE RECEPTOR MEDIATES VARIOUS
-|- FUNCTION: THE MUSCARINIC ACEPTICHINE RECEPTOR MEDIATES VARIOUS
-|- FUNCTION: THE MUSCARINIC ACEPTICHINE RECEPTOR MEDIATES VARIOUS
-|- FUNCTION OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Braun T., Schofield P.R., Shivers B.D., Pritchett D.B., Seeburg P.H., "A novel subtype of muscarinic receptor identified by homology
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-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Furuta M., Ohya S., Imaizumi Y., Watanabe M.;
"Molecular cloning of m3 muscarinic acetylcholine receptor in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wess J., Gdula D., Brann M.R.;
"Site-directed mutagenesis of the m3 muscarinic receptor:
identification of a series of threonine and tyrosine residues
involved in agonist but not antagonist binding.";
EMBO J. 10:3729-3734(1991).
                                                                                                             MEDIINE=90166521; PubMed=3272174;
Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
"Cloning and expression of the human and rat m5 muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 149:125-132(1987).
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PRINTS; PR00237; GPCRHDODPN:
PROSITE; PS00237; GPROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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EMBL; M16408; AAA40662.1; ALT_SEO.
EMBL; M18088; AAA40659.1; -.
EMBL; AB017656; BAA36839.1; -.
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MEDLINE=88077068; PubMed=3120722;
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Neuron 1:403-410(1988).
Science 237:527-532(1987).
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PIR; A29476; A29476.
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Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSTILIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Sukaryota metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
A -> R (IN REF. 4).
C -> R (IN REF. 4).
T -> M (IN REF. 3).
T -> M (IN REF. 3).
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               receptor.
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MEDILINE-94339178; PubMed-8061048;
Lee P.H., Hodges P.K., Glickman F., Chang K.J.;
"Cloning and expression of a cDNA encoding bovine muscarinic
                                                                                                                                                                                                                                                                                                                                                                            67.8%; Score 40; DB 1; Length 589; 71.4%; Pred. No. 38;
                                               CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
            Phosphorylation; Multigene family; G-protein coupled re
DOMAIN 1 66 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Muscarinic acetylcholine receptor M3.
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Biochim. Biophys. Acta 1223:151-154(1994).
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Matches 5; Conserv
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P41984;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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A -> G (IN REF 2)
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16-0CT-2001 (Rel. 40, Last annotation update)
Muscarinic acetylcholine receptor M3.
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01-OCT-1989 (Rel. 12, Last seq
16-OCT-2001 (Rel. 40, Last anno
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                                                                                                 FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENTARE CYCLASE, BREAKDOWN OF PHOSPHOTNOSTITIES & MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
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         MEDILINE-88296835; PubMed-3402600; Akiba I., Kubo T., Maeda A., Bujo H., Nakai J., Mishina M., Numa S.; "Primary Structure of porcline muscarinic acetylcholine receptor III and antagonist binding studies."; FEBS Lett. 235.257-261(1988).
                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                              GCRD; GCR_0104; -.
InterPro: TPR0002; TPR0025.
Pfam: PF00001; 7tm_1; 1.
PRINTS: PR00237; GPCRRHODOPSN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS00265; G_PROTEIN_RECEP_F1_2; 1.
PROSIDE: PS00265; G_PROTEIN_RECP_F1_2; 1.
PROSIDE: PS00265; G_PROTEIN_RECEP_F1_2; 1.
PROSIDE: PS00265; G_PROTEIN_RECEP_F1_2; 1.
PROSIDE: PS00265; G_PROTEIN_RECP_F1_2; 1.
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(Rel. 35, Last sequence update)
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Marchantiales; Marchantiaceae; Marchantia.
                                                                                                                                                                                                                                                                                                                                         "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.PNEUMONIAE MPN333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                          Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 741;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 26.5 kDa protein in RPS2 3'region (ORF 228).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1776A96BCF83567F CRC64;
01-WAR-2002 (Rel. 41, Last annotation update)
Hypothetical protein MPN335 (F10_orf741).
MPN335 OR MP501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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POTENTIAL.
POTENTIAL.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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InterPro; IPR00188; GABAA_receptor.
Pfam; PF02932; Neur_chan_memb; 1.
Hypothetical protein; Transmembrane;
TRANSMEM 34 54 POTENTIA
TRANSMEM 76 96 POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
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milarity 71.4%;
Conservative 0
                                                                                                                                    Mycoplasmataceae; Mycoplasma
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96
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Best Local Similarity
'.'... 5; Conserve
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715
741 AA;
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                                                                                                                                                             NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-95291429; PubMed-7773384;
Vasseur V.V., van Montagu M.M., Goldman G.G.H.;
"Trichoderma harzianum genes induced during growth on Rhizoctonia
                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBL_TaxID=5544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 solani cell walls.";
Microbiology 141:767-774 (1995).
-!- SUBCELLULA LOCATION: Integral membrane protein.
-!- INDUCTION: DURING MYCOPARASITISM.
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1; Length 228;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                      EMBL, M68929; AAC09463.1; -.
PIR; $26009; $26009.
Mendel; 2116; Marpo; ymf5;1.
InterPro; IPR002541; CytC_asm.
InterPro; IPR003557; CytC_blog_CcmC.
Pfam; PF01578; CytC_asm; 1.
PRINTS; PR01386; CCMCBIGGNSIS.
Mitochondrion; Hypothetical protein.
SEQUENCE 228 AA; 26461 MW; BF13C3616D6C7D35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport; Anino-acid transport; Transmembrane.
TRANSMEM 72 92 POTENTIAL.
TRANSMEM 99 117 POTENTIAL.
TRANSMEM 176 200 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 AA.
                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Embi, becomes, 183212.
InterPro; IPR002293; AA_rel_permease_1.
TherPro; IPR002027; Amino_acid_permease.
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                                                                                                                                                                                                                                                                                                                                                           66.1%;
62.5%;
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gywgkgyw 8
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
(Cyclodextrin-glycosyltransferase) (CGTase).
                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                               POTENTIAL.
5FB0A806934DB55D CRC64;
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Transferase; Glycosyltransferase; Calcium; Signal.
SIGNAL 1
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InterPro; IPR000461; Alpha_amylase.
InterPro; IPR002044; CBD_4.
InterPro; IPR01284 alpha-amylase; I.
Pfam; PF02806; alpha-amylase_C; I.
Pfam; PF00686; CBD_4; I.
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MEDLINE=87163498; PubMed=2951300;
                                                                                                                                                                                                                                                62850 MW;
                                                                                                                                                                                                                                                                                                                                                        66.1%;
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257
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573 AA;
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P08704;
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CDGT_KLEPN
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Matches
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August 12, 2002, 17:22:13 ; Search time 41.64 Seconds (without alignments) 33.236 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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3: Sp_fungi:*
4: Sp_human:*
5: Sp_huwantebrate:*
6: Sp_mammal:*
7: Sp_hnc:*
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Gapop 10.0 , Gapext 0.5
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59
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q9h1g7 thermoplasm Q9kfw3 bacillus ha Q9h5j0 homo sapien Q9h5j0 homo sapien Q9h5j1 thermoplasm Q34654 bacillus su Q9h1f3 thermoplasm Q9h1f3 pseudomonas Q9f3t0 rhodothermu Q915j3 pseudomonas Q9f3t0 rhodothermu Q915j3 pseudomonas Q9wf1 drosophila Q2ywf1 drosophila Q2ywf1 drosophila Q2h0f5 bacieriopha Q9kb15 bacillus ha Q9kb18 alcaligenes Q9kb18 alcaligenes Q28349 archaeoglob
SUMMARIES	Q9HLG7 Q9KFW3 Q9KFW3 Q9HXA8 Q9HLF3 Q34654 Q9HLF3 Q9FSTQ Q9FSTQ Q9FBB Q9KBB Q9KBB Q9KBB Q9KBB Q9KBB Q9KBB Q9KBB
DB	10 10 10 10 10 10 10 10 10 10 10
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Score	44 64 44444 
Result No.	22 7 7 8 8 8 7 7 9 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Q9emt5 amsacta moo Q9rt39 deinococcus Q9yb1 gallus gall P95462 plectonema Q9ft90 oryza sativ P97420 synechocyst Q9yew6 aeropyrum p Q01150 magnaporthe Q91152 magnaporthe Q91212 magnaporthe Q9121 pasteutococc Q91221 arabidopsis Q91221 arabidopsis Q91221 arabidopsis Q9467 arreptococc Q91221 arabidopsis Q9121 pseudomonas Q4967 arabidopsis Q95249 streptomyce Q12361 saccharomyce Q12361 saccharomyc Q92013 pseudomonas Q91031 rhizobium m Q08939 meriones un Q91041 arabidopsis Q93wk6 arabidopsis Q93wk6 arabidopsis Q93wk6 arabidopsis Q93wk6 arabidopsis Q94w14 mus musculu	PRT; 748 AA.  Created) Last sequence update) Last sequence update) Last annotation update) Last annotation update)  29001; moplasmales; Thermoplasmaceae; cocker S., Lupas A.N., Baumeister W.; thermoacidophilic scavenger Thermoplasma  -: te proteome. '7 73A030A0E217EE39 CRC64; Score 47; DB 17; Length 748; Pred. No. 25; 0; Mismatches 1; Indels 0; Gaps 0;	441 AA.
EMT5 87139 148 40xB1 40xB1 40xB1 8420 8420 8420 1152 1152 1152 1152 1152 1152 1153 1153	ALIGNMENTS  PRT; 748 & Created) Last sequence Last annotatic artinez ML., ocker S., Lupa thermoacidophi	
0000 0000 0000 0000 0000 0000 0000 0000 0000	PRT;  Created) Last seq Last ann Last a	PRT;
100 100 100 100 100 100 100 100 100 100	16, 116, 126, 126, 126, 126, 136, 136, 136, 136, 136, 136, 136, 13	
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STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Stocker S., Lupas A.M., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
acidophilum.";
Nature 407:508 13(2000).

Mature 407:508 12(2000).

EMBL, AL45063; CAC11420.1; -.
InterPro; IPR000914; SBP_bac_5.
Pfam, PF00465; SBP_bac_5.
Pfam, PF00465; SBP_bac_5;
Pfam, PF00465; SBP_bac_5;
SEQUENCE 716 AA; 79869 WW; C772CB204CC440B4 CRC64;
                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0501.601."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 71.4%; Score 44; DB 17; Length 716; Similarity 71.4%; Pred. No. 68; 5; Conservative 1; Mismatches 1; Indels
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NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002819; BAB21080.1;
SEQUENCE 198 AA; 21475 MW; 13F337BABDB9BEFO CRC64;
                                                                                                                             ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
P0501G01.9 PROTEIN.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Similarity 85.7%; Pred. No. 18;
6; Conservative 1; Mismatches 0
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214 GHWGKGEW 221
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, RR027045; BAB1536.1; -.

InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28.4317.4331(2000).

BMBL; APOUSO8; BAB04077.1; -.

InterPro; IPR003818; SCFA_trans.

Pfam; PF02667; SCFA_trans; 1.

Complete proteome.

Complete proteome.

200716161787 AT039 MW; 5387892F64302026 CRC64;
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Ol-WAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ23392 FIS, CLONE HEP17418.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SHORT-CHAIN FATTY ACIDS TRANSPORTER.
                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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SMART; SM00355; BTB; 1.
SMART; SM500355; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS0157; ZINC_FINGER_C2H2_1; 1.
DNA_LAnding; Metal-binding; Zinc-finger.
SEQUENCE 574 AA; 61827 MW; 28C2FF4DB
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                                                                                                                               Bacillus halodurans.
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RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Entlan K.D., Errington J., Fabret C., Ferrail E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kunita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Media N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sorokin A., Tamakoshi A., Tankamat T., Tarkamaru K.,

RA Sorokin A., Tamakoshi A., Tankamat T., Tarkamaru K.,

RA Vlari A., Wambutt R., Wambuch E., Wedler H., Weitzenegger T.,

RA Vlari A., Wambutt R., Wammoch H., Vannae K., Vasamotti A.,

RA Viari A., Wambutt R., Wammoch H., Yamane K., Yasamotti A.,

RA Viari A., Wambutt R., Wammoch H., Yamane K., Pasumoto K., Yata K.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Voshikawa H., Danchin A.;

RTH complete genome sequence of the gram-positive bacterium Bacillus

RTH complete grane enguence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wambutt R., Wedler H., Lapidus A., Sorokin A., Ehrlich D., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF006665; AABB1166.1;
EMBL; AF015775; AAB72056.1;
                                                                                                                                                                                      Last sequence update)
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                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
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                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
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STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
MEDLINE-2043737; Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20576172; pubMed=11133964; Sarres C.M., Teixeira M.; Santana M., Pereira M.M., Ellas N.P., Soares C.M., Teixeira M.; Gene cluster of rhodothermus marinus high-potential iron-sulfur protein:oxygen oxidoreductase, a caa3-type oxidase belonging to the superfamily of heme-Copper Oxidases."; J. Bacteriol. 183:687-699(2001).

EMBL, AJ249578; CAC08530.1; -..
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                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen.";
Nature 406:959-964(2000).
BEBL; AEGO4892; AAG08179.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 187 AA; 21281 MW; 8908E9EBEE51897 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 31.4 KDA PROTEIN.
Rhodothermus marinus (Rhodothermus obamensis).
Bacteria; CFB group; Rhodothermus group; Rhodothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73CF0EF4970E1E7A CRC64;
                                                                                                                                                                                         Last sequence update)
Last annotation update)
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0
                                                                                                                                           187 AA.
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Pred. No. 20;
0; Mismatches
    Mismatches
                                                                                                                                   O9HV15,
O9HV15,
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last seq
O1-OCT-2001 (TrEMBLrel. 18, Last ann
HYPOTHETICAL PROTEIN PA4793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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277 AA; 31355 MW;
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87.58;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.7
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GYWG-GYW 115
                                                53 GYWG-GYW 59
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                                1 gywgkgyw 8
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SEQUENCE 27
                                                                                                                                                                                                                                                                               Pseudomonas
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Length 277;

DB 2;

Score 43;

72.98;

Query Match

Score 43.5; DB 16; Length 83; Pred. No. 8.4;

73.78; 87.58;

Query Match Best Local Similarity

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Conservative
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DNA Res. 6:83-101(1999).
                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                             329 WGRGYW 334
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STRAIN-ATC: (1562) 7 PAO1;
MEDLINE-2043737; PubMed-10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.U., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulzen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.T., Ankal A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.T.I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pred. No. 46;
0; Mismatches 2; Indels
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 358 AA; 40019 MW; 035673ABE6EDDA58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 51.1 KDA PROTEIN APE1820.
                                                                                                                      01-535 AA. 0015.330 AA. 0015.330 AA. 01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-0CT-2001 (TrEMBLrel. 18, Last annotation update) HYPOTHETICAL PROTEIN PA0736.
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            Mismatches
  Pred. No.
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             5,
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75.0%;
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Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:959-964(2000).
             5; Conservative
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                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 GTWGGGYW 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aeropyrum.
NCBI_TaxID=56636;
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                                                                                                                                                                                                                                 NCBI_TaxID=287;
                                   2 ywgkgyw 8 : | | | | | | |
                                                         3 WWGKGWW 9
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01-NOV-1999
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Q9YAX5
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RX MEDLINE-ROUND N.A.

RX MEDLINE-20196006; Pubbed-10731132;
RA Adams M.D. Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Andams M.D., Celniker S.E., Richards S., Ashburner W., Henderson S.N.,
Sutton G.G., Wortuan J.R., Yandell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortuan J.R., Yandell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortuan J.R., Yandell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortuan J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Baxter E.G., Helt G., Champer M., Pfeiffer B.D.,
RA ADRIL J.F., Agbayoni A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA ADRIL J.F., Agbayoni A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxdelle J., Baytarkaroglu L., Beasley E.M.,
RA Ballew R.M., Baxdelle J., Baytarkaroglu L., Beasley E.M.,
RA Ballew R.M., Baxdelle J., Baytarkaroglu L., Beasley E.M.,
RA Ballew R.M., Baxdelle J., Baytarkaroglu L., Beasley E.M.,
RA Ballew R.M., Baxdelle J., Baytarkaroglu L., Beasley E.M.,
RA Ballew R.M., Baxdelle J., Baytarkaroglu L., Beasley E.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Daviss P.,
RA Borkow D., Botchan M.R., Bouck J., Broketein P., Brotters P., Chandra I.,
RA Ballos B., Deloher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Ballos B., Carrier G., Ferriac S., Rerischmann W.,
RA Barlis N.J., Harvey D., Helman T.J., Well M.-H., Ibeywan C.,
RA Harris N.L., Harvey D., Helman T.J., Well M.-H., Ibeywan C.,
RA Harris N.L., Harvey D., Helman T.J., Well M.-H., Ibeywan C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rimmel B.E., Kodira C.D., Karpfer C., Morris J., Moshrefi R.,
Rahner B.E., Mcdira C.D., Karpfer C., Morris J., Moshrefi R.,
Rahner K., Ramington K.A., Nixon K., Nusskern D.R., Parl Y.,
Randracolo M., Pittman G.S., Pan S., Pollard J., Moshrefi R., Spier E., Spreadling A.C., Staplecho M., Strong K., Wan S., Shen H.,
Randrack R., Woodeage T., Worter E., Wang S., Yano Q., Zhan R.,
Randrack R., Woodeage T., Worter E., Wang S., Zhan R., Zhan R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Merazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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Pred. No. 62;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             27CA636B23A7FF7B CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                       al protein; Complete proteome.
470 Aa; 51138 MW; 27CA636B2
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EMBL, AP000062; BAA80823.1; -.
EMBL, AP000062; BAA80823.1; -.
InterPro; IPR000471; FAD_Gly3P_dh.
InterPro; IPR000045; NAD_binding.
PRINTS; PR01001; FADG3PDH.
PROSTE; PS01289; BHZ; 1.
PROSTHE; PS01289; BHZ; 1.
SEQUENCE 470 AA; 51138 MW; 27CA6
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                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%;
83.3%;
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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                            7
                 Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fuji F., Hirar
Horikoshi K.;
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Q9F189;
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Matches
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Q9F189
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MEDILINE-98043537; Pubmed-9383189;
Chandry P.S., Moore S.C., Boyce J.D., Davidson B.E., Hillier A.J.;
"Analysis of the DNA sequence, gene expression, origin of replication and modular structure of the Lactococcus lactis lytic bacteriophage
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chandry P.S., Moore M.C., Boyce J.D., Davidson B.E., Hillier A.J.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF011378; AAB70078.1; -. Hypothetical protein.
SEQUENCE 133 AA; 15682 MW; 7D985B5C51E961BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage skl.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=31532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                  ;
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                                                                                                                                                                      71.2%; Score 42; DB 5; Length 126; 71.4%; Pred. No. 22;
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                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287.2185-2195(2000).
EBMEL, AD51602, AB51196.1;
FlyBase; FB900037352; CG14673.
SEQUENCE 126 AA; 14140 MW; DC68AB3DFIF5F820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              021906;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 15.7 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 9;
Pred. No. 23;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   133 AA.
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                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.2%; Scu.
100.0%; Pre
0; '
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                                                                                                                                          Query Match
Best Local Similarity 71.4%,
Thea 5; Conservative
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SEQUENCE FROM N.A.
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.", Mucleic Acids Res. 28:4317-4331(2000).

EMBL, APO01511, BAB050019.1. - .

InterPro; IPR000182: Acetyltransf_GCN5.
Pfam, PF00583; Acetyltransf_1.

Complete proteome.

SEQUENCE 180 AA; 20375 MW; 100D7285E880BCEB CRC64;
                                                                                                                                                                                                                                                                                   Gaps
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EMBL; APO01514; BABD5840.1; ...
InterPro; IPR000182; Acetyltransf_GCN5.
Pfam; PF00583; Acetyltransf; 1.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
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BH2121.
BH2121.
Bacillus Halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
CEL_TaxID=86665;
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SEQUENCE FROM N.A.
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RC STRAIN=335T;

RA Hinner I.-S., Buerger S., Schloemann M.;

RT "Characterization of a second gene cluster coding for enzymes of a catechol catabolism in Ralstonia entropha 335T.";

RI Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

BL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL, AF0424023.1; -.

DR FEMBL, AF0424023.1; -.

DR FAMP, PF02667; SCFA_trans. 1.

KW Hypothetical protein.

SQ SEQUENCE 446 AA; 47785 MW; 7CDA57669C3CE0A5 CRC64;

Query Match

Query Match

Atches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps O;

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| Db 49 wgkGFW 54

Search completed: August 12, 2002, 17:28:14
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APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS DOS TEXT
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. STREET: 9th Floor, East Tower CITY: WASHINGTON, D.C. STATE: COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB;
Pred. No. 24;
2; Mismatches
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FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/APF/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08860174A Patent No. 5989830 GENERAL INFORMATION:
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ilarity 75.0%;
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Sequence 12, Appl
Sequence 10, Appl
Sequence 27, Appl
Sequence 24, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 99, Appl
Sequence 22, Appl
Sequence 23, Appl
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Sequence 27, Appl
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9.123 Million cell updates/sec
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                                                                                                                                            August 12, 2002, 17:18:53; Search time 21.42 Seconds
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| Cg012_6/ptodata/2/laa/5A_COMB.pep:*
| Cg012_6/ptodata/2/laa/5B_COMB.pep:*
| Cg012_6/ptodata/2/laa/6A_COMB.pep:*
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-860-174A-12

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US-08-469-202-28

US-08-484-434C-34

US-08-484-434C-34

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US-08-135-135-25

US-08-135-135-25

US-08-135-135-25

US-08-1398-612A-22

US-08-398-612A-22

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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
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US-08-947-965-78

Sequence 78, Application US/08947965A

Sequence 78, Application US/08947965A

Patent No. 6004790

GENERAL INFORMATION:
APPLICANT: Dijkhuizan, Lubbert
APPLICANT: Dijkhuizan, Lubbert
APPLICANT: Dijkhuizan, Carsten
APPLICANT: Osten, Carsten
APPLICANT: Osten, Carsten
APPLICANT: Osten, Carsten
TITLE OF INVENTION: Variants
TITLE OF INVENTION: Variants
FILE REFERENCE: 4285.204-02

CURRENT FILING DATE: 1997-10-09

EARLIER APPLICATION NUMBER: 0477/95

EARLIER APPLICATION NUMBER: 1173/95

EARLIER APPLICATION NUMBER: 1281/95

EARLIER FILING DATE: 1995-10-17

EARLIER FILING DATE: 1995-11-16

EARLIER FILING DATE: 1995-11-16

EARLIER FILING DATE: 1996-04-22

NUMBER OF SEQ ID NOS: 78

LENGTH: 624

LENGTH: 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.8%; Score 40; DB 2; Length 282; 75.0%; Pred. No. 45; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%; Score 39; DB 3; Length 624 ilarity 62.5%; Pred. No. 1.3e+02; Conservative 2; Mismatches 1; Indels
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CRARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
                                                                                                                   APPLICATION NUMBER: US/08/860,174A FILING DATE: June 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-469-202-27
; Sequence 27, Application US/08469202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Klebsiella pneumoniae
US-08-947-965-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-860-174A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GYYGKGYF 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Pred. No. 44;
2; Mismatches 0; Indels
                                                                                                                                 APPLICANT: DAVIS, Paul James
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: VERHOEIJEN, Martine Elisa
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UNILED CONTRY
ZIP: ZOODS-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS TEXT
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: Addust 14, 1996
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GAPPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, COCNELLS Paul Erik
APPLICANT: VERHOELJEN, MATTINE Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP STREET: 1100 New York Avenue, N.W. STREET: 9th Floor, East Tower CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-860-174A-10; Sequence 10, Application US/08860174A; Patent No. 5989830
                                                                     Sequence 12, Application US/08860174A
Patent No. 5989830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.8%; Scc.
75.0%; Pred
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 274 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
COUNTRY: UNITED STATES
ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-860-174A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GYYGKGYF 129
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                                                  US-08-860-174A-12
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Gaps
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ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
SOFFWARE: Patentin Release #1.0, Version #1.25
CORFUTER: Patentin Release #1.0, Version #1.25
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,434C
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/016,881
FILING DATE: 11-FEB-1993
CTASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Patent No. 5969214
GENERAL INFORMATION:
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene LLC
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 655; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
COMPUTER: Apple Macintosh
OPERATING SYGTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,202
FILING DATE: 6-JUNE-95
CLASSIFTCATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/016,881
FILING DATE: 1, FEB_193
CLASSIFTCATION BOTA:
APPLICATION NUMBER: 31,845
NAME: Blizabeth Lassen
REGISTRATION NUMBER: 34,719
NAME: Blizabeth Lassen
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 36,924
REFERENCE/JOCKET NUMBER: 36,924
REFERENCE/JOCKET NUMBER: 36,924
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 36,924
REFERENCE/JOCKET NUMBER: 36,924
REFERENCE/JOCK
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ATTORNEY/AGENT INFORMATION:
NAME: Schwedler, Carl J.
REGISTRATION NUMBER: 36,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 655 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.1
Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GYWGRDYF 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-469-202-28
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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   Patent NO. 5750875
GENERAL INFORMATION:
APPLICANT: STALKER, DAVID
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/08469202
Petent No. 5750875
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: CALGENE, INC.
STREET: 1920 FIFTH STREET
CITY: DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%; Score 39; DB 1; Length 655; 62.5%; Pred. No. 1.4e+02; 1ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,202
FILING DATE: 6-JUNE-95
CLASSIFCATION NUMBER: 08/016,881
FILING DATE: 11 FEB_193
CLASSIFCATION NUMBER: 31,845
NAME: Blizabeth Lassen
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
REFERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
                                                                                                                                                                                                                                   ADDRESSEE: CALGENE, INC.
STREET: 1920 FIFTH STREET
CITY: DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSS: single
linear
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GYWGRDYF 129
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; HYPOTHETICAL:
US-08-469-202-27
                                                                                                                                                                                                                                                                                                                                                                 <u>۲</u>
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US-08-469-202-28
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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GENERAL INFORMATION:

APPLICANT: MAAT, JAN

APPLICANT: MUSTERS, WOUTER

APPLICANT: STAM, HEIN

APPLICANT: SCHAAP, PETER J.

APPLICANT: SCHAAP, PETER J.

APPLICANT: VISSER, JACOB

APPLICANT: VISSER, JACOB

APPLICANT: VISSER, JOHANNES M.

TITLE OF INVENTION: RIPENING FORM OF A POLYPEPTIDE HAVING SULFHYDRYL OXIDASE

TITLE OF INVENTION: ACTIVITY

NUMBER OF SEQUENCES: 14

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: BUSSEY, HOWARD; BOONE, CHARLES; SOMMER, STEVE S.;
HILL, KATHRYN; MEADEN, PHILIP
HILL, ATHRYN; MEADEN, PHILIP
TILLE OF INVENTION: GENES WHICH PARTICIPATE IN B-GLUCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.4%; Score 38; DB 1; Length 392; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/423,441
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/044,620
FILING DATE:
CLASSIFICATION NUMBER: US 08/044,620
FILING DATE:
PATORNEY/AGENT INFORMATION:
NAME: KORULIS, PAUL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16773
HER: 202744/T7019(V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTORANT PAGENT FROM THE AND T
                                                                                                                                                                                                                                                                            Sequence 2, Application US/08423441 Patent No. 5529926
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; MOLECULE TYPE: protein
US-08-423-441-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WASHINGTON STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                          1 gywgkgyw 8
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122 GYWGRDYF 129
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5194600-4
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COMPUTER: IBM PC
OPERATING SYSTEM: Windows NT 4.0; MS Word for Windows 7.0a
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/484,434C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA: 08/016,881
FILING DATE: 11-FBB-1993
CLASSIFICATION: 800
CLASSIFICATION: 800
CLASSIFICATION: 800
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TITLE OF INVENTION: GLYCOGEN BIOSYNTHETIC ENZYMES IN PLANTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene LLC
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.1%; Score 39; DB 2; Length 655; Best Local Similarity 62.5%; Pred. No. 1.4e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2; Length 655; Pred. No. 1.4e+02; 2; Mismatches 1; Indels
REFERENCE/DOCKET NUMBER: 15593/01
TELECOMMUNICATION INFORMATION:
TELEPAX: 530-792-2463
TELEPAX: 530-792-2463
TELEPAX: 530-792-2463
TELEPAX: 650-792-2463
TELEPAX: 655 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Schwedler, Carl J.
REGISTRATION NUMBER: 36,924
REFERNCE/DOCKET NUMBER: 15593/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 530-792-2265
TELEFAX: 530-792-2463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-484-43C-35
; Sequence 35, Application US/08484434C
; Detent No. 5969214
; GENERAL INFORMATION:
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62.5%;
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LENGTH: 655 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.19
Best Local Similarity 62.59
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 95616
COMPUTER READABLE FORM:
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STATE: CA
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Sequence 99, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 296, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ANDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                           ADDRESSEE: William M. Smith
STRET: One Market Plaza, Steuart Tower, Suite 2000
STRET: Can Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TERRES FLORM:
MEDIUM TERRES FLORPY disk
COMPUTER: FLORPY disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2;
Pred. No. 15;
1; Mismatches
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FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERNEK/COCKET NUMBER: 14643-9-1-
TELEPHONE: 415-326-2400
FILEPHONE: 415-326-2420
FILEPHONE: 415-326-2422
FILEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FENCHH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14643-9-1-1
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-308-865-99
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California
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GYWGQG 18
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Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                Score 38; DB 6; Length 1365;
Pred. No. 3.9e+02;
1; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IS Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/853,408B

FILING DATE: 19920318

CLLASSIFRCATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 14643-9

TELECOMMUNICATION INFORMATION:

TELEFHONE: 415-326-2400

THENDRAME FOR SECOND FOR S
                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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1; Mismatches
                        NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,316
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                          64.48;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTER.STICS: LENGTH: 29 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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STATE: California
; ASSEMBLY AND USE THEREOF
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                        ; SEQ ID NO:4:
; LENGTH: 1365
5194600-4
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US-07-853-408B-99
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US-08-308-865-99
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Length 29; Indels ဖ

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CURRENT TYPE: Floppy disk

OMEDITAR: ISTAN PROF FORDS/MS-DOS

SUFFWARE: Datentin Rolls Proposition #1.30

CURRENT PROPISATION DATA:
PRICE CONTRACTOR TO THE PROPISATION PROPISATION DATA:
PRICE APPLICATION BARN: 1998

CLASSILICATION BARN: 1998

FILING DATE: 18 HAR-1992

PRICE APPLICATION DATA:
PRICE APPLICATION DATA:
PRICE APPLICATION DATA:
PRICE APPLICATION DATA:
PRICE APPLICATION MURBER: US 07/894,068

PRICE APPLICATION DATA:
PRICE APPLICATION NUMBER: UO COCT-1995
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Gaps AL INFORMATIONS:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies ö Score 37; DB 4; Length 29; Pred. No. 15; 1; Mismatches 0; Indels COUNTRY: USA
ZIP: 94111-388
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California · ATTORNEY/AGENT INFORMATION:
NAME: SCREAfin1, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DC-1996
CLASSIFICATION NUMBER: US/08/728,463
PELLING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/728,463
PELLING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/35,322
FILING DATE: 10-DEC-1994
APPLICATION NUMBER: US 08/35,322
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/16,739
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,301
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/15,301
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 08/096,762
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 08/096,762
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 08/096,762
FILING DATE: 16-DEC-1992 ; TOPOLOGY: Linear ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 144: US-08-758-417A-144 Sequence 144, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION: TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS: TYPE: amino acid STRANDEDNESS: <Unknown> Conservative Best\_Local Similarity Matches 5; Conserv 13 GYWGQG 18 1 gywgkg 6 RESULT 14 US-08-758-417A-144 Query Match ò q

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Job time: 197 sec
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                      Gaps
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0
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0
    62.7%; Score 37; DB 4; Length 29; 83.3%; Pred. No. 15; 0; Indels live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.7%; Score 37; DB 1; Length 30; Best Local Similarity 83.3%; Pred. No. 15; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 30 amino acids TYPE: amino acid
    Query Match 62.7
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-053-131-99
                                            13 GYWGQG 18
                                 1 gywgkg 6
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Search completed: August 12, 2002, 17:22:10

Mon. 2ug 12 17:16:32 2002

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Compugen Ltd.
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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OM protein - protein search, using sw model

August 12, 2002, 17:22:44; Search time 27.08 Seconds (without alignments) 28.387 Million cell updates/sec Run on:

10-071247-2 66 Perfect score:

1 cywgcgyw 8 Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

P.	saposin precursor hypothetical prote hypothetical prote relaxin - horse (f relaxin B,C and A hypothetical prote hypothetical prote hypothetical prote N-acetylgalactosam N-acetylgalactosam N-acetylgalactosam probable glycogen hypothetical prote late embryogenesis integral membrane muscarinic acetylc muscarinic acetylc muscarinic acetylc muscarinic acetylc hypothetical prote hypothetical prote hypothetical prote polyprotein - marm ig heavy chain V hypothetical prote
ıs o	A28/16 E96704 A46430 A46430 147053 147053 131755 T31755 T31755 T31755 T31756 B29514 A29476 A29476 A29476 A21810 S73827 A71810 S73827 A74809 T4809 T4809 T4809 T4809 T4809
DB	
gth	2569 483 483 484 483 485 486 486 486 486 486 486 486 486 486 486
$^{r}$	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
* OX	
Score	
Result No.	22222222222222222222222222222222222222

saposin precursor	INDAL Protein · iu angiotensin-conver maior high-(glycin	hypothetical prote conserved hypothet	probable dCTP deam	probable prospinces nitrogenase (EC 1.	hypothetical prote oxidoreductase (EC	inositol-1,4-bisph	nypornetical proce nitrogenase (EC 1.	nitrogenase molybd
SAHUP JH0604	S33212 JC5374 KRSHI6	H84004 A69846	H72759	S50136	T38935 AF3304	A39254	TUSE64 NIAIMA	AF1986
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527	573 630 62	116	163	304	317	400	4 6 6 4 8 0	497
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30 31	3 8 8 2 8 9 8	35 36	37	36 36	40 41	42	4 4 4 4	45

## ALIGNMENTS

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saposin precursor - rat N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon ein (SAP): sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulf N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

Cydcossion: A28716
RCCollard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.
RCCollard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.
Blochemistry 27, 4557-4564, 1988
A.Title: Blosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by ra A;Reference number: A28716; MUID:89000647
A;Reference number: A28716; MUID:89000647
A;Residues: 1-554 <COL>
A;Residues: 1-54 <COL>
A;Residues: 1-54 <COL>
A;Residues: 1-54 <COL>
A;Residues: 1-554 <

C;Function:
A;Description: Saposins bind sphingolipids, form hydrophilic complexes and make them A;Pathway: sphingolipid catabolism
A;Desthway: sphingolipid catabolism
A;Note: saposins A and C (SAP-2) activate hydrolysis of galactocarebroside by beta-gluc A;Note: saposin B (SAP-1) activates hydrolysis of sphingomyelin by sphingomyelin by aryls A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiest C;Superfamily: saposin; saposin repeat homology
C;Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; F;1-16/Domain: signal sequence #status predicted <SIG>F;1-16/Domain: saposin repeat homology <SAPI>F;1-16/Domain: saposin repeat homology <SAPI>F;1-18/Domain: saposin pepat homology <SAPI>F;1-18/Domain: saposin repeat homology <SAPI>F;1-18/Domain: saposin pepat homology <SAPI>F;1-18/Domain: saposin pepat homology <SAPI>F;1-18/Domain: saposin pepat homology <SAPI>F;1-18/Domain: saposin repeat homology <SAPI>F;1-18/Domain: saposin pepat homology <SAPIDIA (SAPIDIA) (SAPIDI

ö Gaps ö Score 46; DB 1; Length 554; Pred. No. 17; 0; Mismatches 2; Indels 69.78; Query Match
Best Local Similarity 75.0
Matches 6; Conservative

525 CVWGPGYW 532 1 cywgcgyw 8 Db δλ

RESULT E96704

a

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A;Map position: 5
A;Introns: 66/3; 122/2; 167/2; 214/3; 319/1
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Best Local Similarity 100..
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Best Local Similarity 100.
Matches 5; Conservative
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Nature 408, 816-820, 2000
A; Muthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A; Molecule type: DNA
A; Residues: 1-283 <STO>
A; Cross_references: GB: AE002093; NID: 96598329; PIDN: AAF18588.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-269 <STO>
A;Cross-references: GB:AE005173; NID:96553884; PIDN:AAF16550.1; GSPDB:GN00141
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C;Species: Equus caballus (domestic horse)
C;Species: Hquis caballus (domestic horse)
C;Apte: 07-Apr-1994 # sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: B49739; A49739
R;Stewart, D.R.; Nevins, B.; Hadas, E.; Vandlen, R.
Endocrinology 129, 375-383, 1991
hypothetical protein T23K23.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45.5; DB 2;
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Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.9%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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A; Status: preliminary
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A;Map position: 2
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A; Gene: T23K23.3
A; Map position: 1
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A,Title: Affinity purification and sequence determination of equine relaxin.
A,Reference number: A49739; MUID:91275796
A,Rocession: B49739; MUID:91275796
A,Molecule type: protein
A,Molecule type: pyrodiutamic acid
C,Seywords: hormone; pyroglutamic acid
C,Seywords: hormone; pyroglutamic acid
F;1-28,79-Molecule Telaxin #status experimental <AMA>
F;1-28,70-Molecule type: pyrodidone carboxylic acid (Gln) (in mature form) #status exper
F;10-34,22-39,35-48/Disulfide bonds: #status predicted
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C; Species: Equus sp.
C; Date: 04-69p-1997 #sequence_revision 07-Nov-1997 #text_change 16-Jul-1999
C; Date: 04-69p-1997 #sequence_revision 07-Nov-1997 #text_change 16-Jul-1999
C; Accession: 147053
B; Klonisch, T.; Ryan, P.L.; Yamashiro, S.; Porter, D.G.
Biol. Reprod. 52, 1307-1315, 1995
A; Title: Partial complementary decxyribonucleic acid cloning of equine relaxin messen
A; Reference number: 147053; MUID: 95359320
A; Restince preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Restinces: 143 < KLO>
A; Cross references: KLO
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A;Experimental source: strain Bristol N2; clone C07G3
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31757
R;Geisel, C.; Wamsley, P.
Submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C07G3.
A;Reference number: 221080
A;Accession: T31757
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
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9.6;
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hypothetical protein C07G3.3 - Caenorhabditis elegans
C:Species: Genorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Co-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C;Accesion: T3158
R;Geisel, C.; Wamsley, P.
Submitted to the RMLD Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C07G3.
A;Reference number: 221080
A;Reference number: 221080
A;Geression: T3158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Geresidues: 1351
A;Molecule type: DNA
A;Residues: 1351
A;Gens: ERBL:AF016432; PIDN:AAB65377.1; GSPDB:GN00023; CESP:C07G3.3
A;Experimental source: strain Bristol N2; clone C07G3
A;Gene: CESP:C07G3.3
A;Map position: 5
A;Introns: 66/3; 122/2; 167/2; 214/3; 319/1
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A:Experimental source: strain Bristol N2; clone C07G3
C:Genetics:
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hypothetical protein C07G3.6 - Caenorhabditis elegans
hypothetical protein C07G3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31755
R;Geisel, C.; Wamsley, P.
R;Geisel, C.; Wamsley, P.
R;Geisel, C.; Wamsley, P.
R;Geisel, C.; Wamsley, Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C07G3.
A;Reference number: Z21080
A;Reference number: Z21080
A;Reference number: Z31080

                                                                                                   Gaps
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                              Length 342;
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                              Score 42; DB 2;
Pred. No. 44;
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Pred. No. 44;
0; Mismatches
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                                                                                                Mismatches
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A;Introns: 66/3; 122/2; 167/2; 214/3; 319/1
63.6%; Scc.
100.0%; Pre
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ilarity 100.0%;
Conservative 0
                                                                                         5; Conservative
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Best Local Similarity
'-has 5; Conservē
                        Query Match
Best Local Similarity
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Matches 5; Conserv
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97 CYWGC 101
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Aritie: Micopolyaccharidosis type VI in rats: Isolation of cDNAs encoding arylsulfa A; Reference number: 154210; MUID:96121368
A; Accession: 154210
A; Accession: 154210
A; Molecule type: mRNA
A; Residues: 1-473 < RES>
A; Residues: 1-473 < RES>
A; Cross-references: GB:D49434; NID:91065603; FIDN:BAA08412.1; PID:91089794
C; Genetics:
A; Conetics: C; Superfamily: animal sulfatase
C; Superfamily: animal sulfatase
C; Superfamily: animal sulfatase
C; Superfamily: animal sulfatase
C; Reywords: sulfuric ester hydrolase
F; 31/Modified site: 3-oxoalanine (Cys) #status predicted
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A. Residues: 1-533 < PET>
A. Molecule type: DNA
A. Residues: 1-533 < PET>
A. Molecule type: DNA
A. Residues: 1-533 < PET>
A. Cross-references: BMBL:X72735; NID:9289009; PIDN:CAA51272.1; PID:9825628
B. Modaressi, S.: Rupp, K.; von Figura, K.; Peters, C.
Biol. Chem. Hoppe-Seyler 374, 327-335, 1993
A. Title: Structure of the human arylsulfatase B gene.
A. Reference number: S33307; MUID:93332648
A. Accession: S33307
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: BMBL:X72735; EMBL:X72736; EMBL:X72737; EMBL:X72738; EMBL:X72739;
A. Note: the enzyme is referred to as EC 3.1.6.9
B. Peters, C.; Schmidt, B.; Rommerskirch, W.; Rupp, K.; Zuehlsdorf, M.; Vingron, M.; M
A. Title: Phylogenetic conservation of arylsulfatases. CDNA cloning and expression of A. R. Reference number: A35078; MUID:90153994
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A. Residues: 1-357, 'V' 359-533 cPE2>
A. Cross-references: GB.J05225; NID:q179076; PIDN:AAA51784.1; PID:q179077
A. Wote: parts of this sequence were determined by protein sequencing
A. Note: parts of this sequence were determined by protein sequencing
A. Note: the enzyme is referred to as EC 3.1.6.1
A. Mote: the enzyme is referred to as EC 3.1.6.1
B. Lochem. Int. 24, 209-215, 1991
A. Title: Human N-acetylgalactosamine-4-sulphatase: protein maturation and isolation o
A. Reference number: A45659; MUID:92028992
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N-acetylgalactosamine-4-sulfatase (EC 3.1.6.12) precursor - rat (fragment) N;Alternate names: arylsulfatase (EC 3.1.6.1) B [misidentification] C;Species: Rattus norvegicus (Norway rat) C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 02-Jun-2000
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A;Residues: 1-104 <LIT>
A;Cross-references: GB:S57777; NID:g236697; PIDN:AAB19988.1; PID:g236698
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Pred. No.
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ilarity 85.7%;
Conservative
                                                                                                                                         C, Accession: 154210
R; Kunieda, T.
Genomics 29, 582-587, 1995
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Best Local Similarity
Matches 6; Conserv
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Circession: D70770
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brovies, R.; Pevilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; Mulb:98295987
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A;Experimental source: strain MSB8
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A;Experimental source: strain H37Rv
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A;Accession: B72392
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                  probable glycogen phosphorylase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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89;
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            Mismatches
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71.4%;
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nes 4; Conservative
            6; Conservative
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Nature 399, 323-329, 1999
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A; Residues: 1-83 <ARN>
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A;Gene: TM0315
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A; Accession: C42449
A; Accession: C42449
A; Accession: C42449
A; Molecule type: mRNA
A; Resaldues: Manna
A; Accession: C42449
A; Molecule type: mRNA
A; Resaldues: GB: S90743; NID: G47490; PIDN: AAB21833.1; PID: G247491
A; Note: Accession: C4249
A; Title: A novel anino acid modification in sulfatases that is defective in multiple sul A; Reference number: A57113; MUID: 95534208
A; Title: A novel anino acid modification in sulfatases that is defective in multiple sul A; Reference number: A57113; MUID: 95534208
A; Contents: annotation; dentification of 3-oxoalanine, 2-amino-3-oxopropanoic acid A; Schuchman, E. H.; Jackson, C. E.; Desnick, R.J.
Genomics 6, 149-158, 1990
A; Title: Human arylsulfatase B: MOPAC cloning, nucleotide sequence of a full-length cDNA; Reference number: 154217; MUID: 90152677
A; Recession: 154217
A; Residues: 1557; VV, 359-375; VV, 377-533 < RES>
A; Status: preliminary; translated from GB/EMBL/DBBJ
A; Molecule type: mRNA
A; Residues: 1:357, VV, 359-375; VV, 377-533 < RES>
A; Cross-references: GB: M32373; MID: 9179029; PIDN: AAA51779.1; PID: 9179030
B; Robayashi, T.; Honke, K.; Jin, T.; Gasa, S.; Miyazaki, T.; Makita, A.
Biochim. Biophys. Acta 1159, 243-247, 1992
A; Reference number: A56665; MUID: 93003385
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A;Map position: 5q11-5q13
A;Introns: 104/3; 167/1; 230/3; 300/1; 381/2; 405/1; 446/1
A;Note: defects in this gene can cause mucopolysaccharidosis type VI, Maroteaux-Lamy dis C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Superciption: hydrolyzes N-acetylgalactosamine-4-sulfate units in chondroitin sulfate a Superfamily: animal sulfatase
C;Superfamily: animal sulfatase
C;Superfamily: animal sulfatase
C;Superfamily: animal sulfatase
C;Superfamily: animal sulfatase
E;1-40/Domain: signal sequence #status predicted <SIG>
F;41-423/Product: alpha chain #status predicted <AMAT>
F;424-465/Product: gamma chain #status predicted <AMAT>
F;466-333/Product: beta chain #status experimental <BNAT>
F;188-279;366,458/Bainding site: carbohydrate (Asn) (covalent) #status predicted
F;291/Bainding site: carbohydrate (Asn) (covalent) #status absent
F;426/Binding site: carbohydrate (Asn) (covalent) #status experimental
A; Note: sequence extracted from NCBI backbone (NCBIN:57777, NCBIP:57778)
A; Note: the enzyme is referred to as EC 3.1.6.1
A; Note: parts of this sequence, including the amino end of the mature protein, were dete A; Note: a form is described with a proteolytic cleavage somewhere between residue 450 an R; Jin, W.D.; Jackson, C.E.; Desnick, R.J.; Schuchman, E.H.
Am. J. Hum. Genet. 50, 795-800, 1992
A; Title: Mucopolysaccharidosis type VI: identification of three mutations in the arylsul
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A; Residues: 41-55; 424-425, XZ, 427-454;466-483 <KOB>
A; Resperimental source: placenta
A; Note: sequence modified after extraction from NCBI backbone
A; Note: the fragments shown are the amino ends of the alpha, gamma, and beta chains of
C; Comment: This enzyme is frequently misidentified as EC 3.1.6.1.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 234.235, Pr, 237-238 <JI2>
A;Residues: 234.235, Pr, 281.590736; NID:g247488; PIDN:AAB21832.1; PID:g247489
A;Cross-reference: GB:S90736; NID:g247488; PIDN:AAB21832.1; PID:g247489
A;Note: sequence extracted from NCBI backbone (NCBIN:90736, NCBIP:90739)
                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 115-116, R', 118 <JIN>
A;Cross-references: GB:S90729; NID:g247486; PIDN:AAB21831.1; PID:g247487
A;Otce: sequence extracted from NCBI backbone (NCBIN:90729, NCBIP:90731)
A;Accession: B42449
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62;
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Pred. No.
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A;Accession: A42449
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Hic

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Gaps

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Indels

Length 863;

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Gaps

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Indels

Length

5;

late embryogenesis abundant M17 protein [imported] - Arabidopsis thaliana

Best Local Similarity

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A.Accession: B94233

A.Molecule type: mRNA

A.Residues: 1-269,463-802>

A.Fexperimental source: cerebral cortex

A.Note: only a part of the protein translation is given; none of the nucleotide seque

R.Kurtenbach, E.; Curtis, CA.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.

J. Biol. Chem. 265, 13702-13708, 1990

A.Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues i

A.Reference number: A37121; MUID:90337982
                                                                                                                                                                                                                                                                                                                                                                                                                      A. Molecule type: protein
A. Residues: 104-166 ckUR>
A. Residues: 104-166 ckUR>
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate rhodopsin
C. Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran
C. Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran
F:07-90/Domain: transmembrane #status predicted <TMA>
F:142-163/Domain: transmembrane #status predicted <TMA>
F:130-251/Domain: transmembrane #status predicted <TMA>
F:230-251/Domain: transmembrane #status predicted <TMA>
F:542-512/Domain: transmembrane #status predicted <TMA>
F:547-545/Domain: transmembrane #status predicted <TMA>
F:6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                     A; Reference number: A94293; MUID:87263421
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Best Local Similarity 71.4%;
Matches 5; Conservative
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A; Status: preliminary
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R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Barton, G.; Omelchenko, M.V.; Smith, D.R.
J.; Barceriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325, PMID:21359325
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Residues: 1-441 < KUR>
A; Residues: 1-441 < KUR>
A; Residues: 1-441 < KUR>
A; Cross-references: GB:AE001437; PIDN:AAK78539.1; PID:g15023427; GSPDB:GN00168
A; Gene: CAC0560
                                                                C; Accession: G84839

K; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A; Reference number: A84420; MUID: 20083487
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A; Residues: 1-589 <BO1>
R; Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A; Title: Identification of a family of muscarinic acetylcholine receptor genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE002093; NID: 93894196; PIDN: AAC78545.1; GSPDB: GN00139
Species: Arabidopsis thaliana (mouse-ear cress)
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000
C;Accession: B94518; B94293; B37121; B29514
S;Bonner, T.I.
submitted to GenBank, July 1987
A;Reference number: A94518
A;Reference number: A94518
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1; Mismatches
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Matches 5; Conserv
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Gaps

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Score 41; DB 2; Length 589; Pred. No. 93; 0; Mismatches 2; Indels

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2002, 17:27:25 ; Search time 13.51 Seconds (without alignments) 22.928 Million cell updates/sec Run on:

10-071247-2 66 Title: Perfect score: Sequence:

1 cywgcgyw 8

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 segs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6 4 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	ULT 1 CHICK SAP_CH 013035 16-OCT 16-OCT 16-OCT Proact Saposi PSAP Gallus Gallus Gallus Gallus	NCBI_1 [1] SEQUEN TISSUE MEDLIN Azuma Paton "Cloni Bloche	Altman Namitten Namit
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SEQUENCE FROM N.A.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                            EMBL; AB003471; BAA19914.1; -

BR EMBL; AF108656; AAF05899.1; -

BR InterPro; IPR003119; SapA.

BR InterPro; IPR003259; Saposin.

R PF02199; SAPA; 2.

R ProDom; PD012321; SapB; 3.

R SMART; SM00163; SaPA; 4.

SMART; SM00118; SAPA; 4.

SIGNAL SIGNAL INSOSOME; Sphingolipid metabolism; Repeat; W GMZ-gangilosidosis.

F SIGNAL SIGNAL SAPA; 1.

SIGNAL SIGNAL SAPA; 2.

SIGNAL SIGNAL SAPA; 2.

SIGNAL SIGNAL SAPA; 3.

SIGNAL SIGNAL SAPA; 4.

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SIGNAL SAPA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD; PRT; 554 AA.
P10960; Q62841; Q04190;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-QCT-2001 (Rel. 40, Last annotation update)
Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
PSAP OR SGP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> T (IN REF. 2).
-> D (IN REF. 2).
B803000E891C3963 CRC64;
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SAPOSIN A.
SAPOSIN B.
SAPOSIN C.
SAPOSIN D.
SAPOSIN D.
SAPOSIN-LIKE TYPE A 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 3.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 2.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Mon Aug 12 17:16:33 2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95359320; PubMed=7543295; Klonisch T., Ryan P.L., Yamashiro S., Porter D.G.; "Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91275796; PubMed-2055195; Stewart D.R., Nevins B., Hadas E., Vandlen R.; Stewart D.R., Nevins B., Hadas E., Vandlen R.; Maffiltoation and sequence determination of equine relaxin."; Endocrinology 129:375-383(1991).

-I. FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.

-I. SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                       0;
                                                                                                                                               DB 1; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                       Indels
                                                                               DFE3F3A3A0520C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lecular cloning of equine preprorelaxin cDNA."; Reprod. Dev. 42:171-178(1996),
  D -> E (IN REF. 2).
I -> V (IN REF. 3).
W -> R (IN REF. 3).
S -> M (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                 P.20565; 028907; 10. Created) 01-AUG-1991 (Rel. 19, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-CCT-2001 (Rel. 40, Last annotation update) Prorelaxin precursor (RXN).
                                                                                                                                                                                                                                                                                                                                                                       182 AA
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                             69.7%; Score 46; 75.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-HOKKAIDO; TISSUE-Placenta;
Min K., Shiota K., Ogawa T.;
"Molecular cloning of equine prep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Reprod. 52:1307-1315(1995).
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                                                                                 61123 MW;
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PIR; A49739; A49739.
PIR; B49739; B49739.
HSSP; P01348; 4RLX.
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse).
299
462
527
536
554 AA;
                                                                                                                                          Query Match
Best Local Similarity
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CONFLICT
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RELX_HORSE
DAC P22969,
DAC P22969,
DT 01-NOG;
DT 01-NOG;
DE PROFELI
GN RELN.
OC EUKARIY,
OC TISSUE
RY MEDLIN
RA KIDDIS
RY MEDLIN
RY SEWBL;
DR EWBL;
DR EWBL;
DR FIRE;
DR FIRE;
DR FIRE;
DR FIRE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mucopolysaccharidosis type VI in rats: isolation of cDNAs encoding arylsulfatase B, chromosomal localization of the gene, and identification of the mutation."; Genomics 29:582-587(1995).

-!- CATALYTIC ACTIVITY: Hydrolysis of the 4-sulfate groups of the N-acetyl-D-galactosamine 4-sulfate units of chondroitin sulfate and dermatan sulfate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: LYSOSOMA1.
-:- DISEASE: DEFECTS IN ARSB ARE THE CAUSE OF MAROTEAUX-LAMY
SYNDROME; ALSO KNOWN AS MUCOPOLYSACCHARIDOSIS TYPE VI (MPS-VI).
-:- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Arylsulfattase B (EC 3.1.6.12) (ASB) (N-acetylgalactosamine-4-sulfatase) (G4S) (Fragment).
                                                                         COUNECTING PEPTIDE.
RELAXIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
A -> V (IN REF. 2).
L -> Q (IN REF. 2).
W, E5C9414303A838B8 CRC64;
                                                                                                                                                                                                                               63.6%; Score 42; DB 1; Length 182; 100.0%; Pred. No. 6.7; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO017; Sulfatase.
Pfam; PF00884; Sulfatase; 1.
PROSITE; PS00523; SULFATASE_1; 1.
PROSITE; PS00149; SULFATASE_2; FALSE_NEG.
Hydrolase; Glycoprotein; Lysosome; Mucopolysaccharidosis.
NON_TER 31 2-AMINO-3-OXOPROPIONIC ACID A
                                                                 RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                      473 AA.
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MEDLINE-96121368; Pubmed~8575749;
                                 Hormone; Signal.
                                                         54 156
61 182
7 182
173 66
133 1
20721 MW;
PROSITE; PS00262; INSULIN; 1. Insulin family; Hormone: Sirvagnar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D49434; BAA08412.1; -. HSSP; P15848; 1FSU.
                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                            26
161
161
35
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168
133
182 AA;
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Best Local Similarity
Matches 5; Conserv
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DISULFID
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P50430;
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Cell 82:271-278(1995)
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MEDDINE-90152677; PubMed=1968043;
Schuchman E.H., Jackson C.E., Desnick R.J.;
Human arylsulfatase B: MoPAc cloning, nucleotide sequence of a full-length cDNA, and regions of amino acid identity with arylsulfatases A
                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-AMY-2000 (Rel. 39, Last annotation update)
Arylsulfatase B precursor (EC 3.1.6.12) (ASB) (N-acetylgalactosamine-4-sulfatase) (G4S).
                                                                                                                                                                           Gaps
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Schnatd B., Selmer T., Ingendoh A., von Figura K.;
"A novel amino acid modification in sulfatases that is defective in
multiple sulfatase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92028992; PubMed-1930244;
Litjens T., Morris C.P., Gibson G.J., Beckmann K.R., Hopwood J.J.;
"Human N-acetylgalactosamine-4-sulphatase: protein maturation and
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                       (POTENTIAL).
                                                                               (POTENTIAL).
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                                                               (POTENTIAL)
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Peters C., Schmidt B., Rommerskirch W., Rupp K., Zuehlsdorf M., Vingron M., Meyer H.E., Pohlmann R., von Figura K.;
"Phylogenetic conservation of arylsulfatases. cDNA cloning and expression of human arylsulfatase B.";
J. Biol. Chem. 265:3374-3381(1990).
                                                                                                                (POTENTIAL)
                                                                                                                                                                           ;
0
                                                                                                                                                       Length 473;
                                                                                                                                                                           Indels
                                                                                                                         4E114C923A24AF8F CRC64;
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          POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC...
                                                                                                                                                      Score 42; DB 1;
Pred. No. 15;
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                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolation of genomic clones.";
Biochem. Int. 24:209-215(1991).
                                                                                                                          MΜ.
                                                                                                                                                       63.68;
85.78;
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                                                                                                                          53320
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                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                         473 AA;
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                  384 YPGCGYW 390
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
           87
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366
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            ACT_SITE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92197625; PubMed-1550123;
MEDLINE-92197625; PubMed-1550123;
Jin W.-D., Jackson C.E., Desnick R.J., Schuchman E.H.;
"Mucopolysaccharidosis type VI: identification of three mutations in
the arylsulfatase B gene of patients with the severe and mild
phenotypes provides molecular evidence for genetic heterogeneity.";
Am. J. Hum. Genet. 50:795-800(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE=92042029; PubMed=1718978; Wicker G., Prill V., Brooks D., Gibson G., Hopwood J., von Figura K., Peters C.; "Mucopolysaccharidosis VI (Maroteaux-Lamy syndrome). An intermediate clinical phenotype caused by substitution of valine for glycine at position 137 of arylsulfatase B."; J. Biol. Chem. 266:21386-21391(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Littens T., Brooks D.A., Peters C., Gibson G.J., Hopwood J.J.;
Lidentification, expression, and biochemical characterization of
acetylgalactosamine-4-sulfatase mutations and relationship with
clinical phenotype in MPS-VI patients.";
Am. J. Hum. Genet. 58:1127-1134(1996).
                        MEDLINE-97184692; PubMed-9032078;
Bond C.S., Clements P.R., Ashby S.J., Collyer C.A., Harrop S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Four novel mutant alleles of the arylsulfatase B gene in two patients with intermediate form of mucopolysaccharidosis VI (Maroteans-Lamy sundrome) ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Voskoboeva E., Isbrandt D., von Figura K., Krasnopolskaya X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS MPS-VI MET-92; GLN-95; CXS-210; PRO-393 AND PRO-498 MEDLINE-96213747; PubMed-8651289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO-3-OXOPROPIONIC ACID.
                                                                                   Hopwood J.J., Guss J.M.; "Structure of a human lysosomal sulfatase."; Structure 5:277-289(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT MPS-VI VAL-137, AND VARIANT MET-376.
CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS MPS-VI TRP-152 AND GLN-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94171224; PubMed=8125475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Maroteaux-Lamy syndrome).";
Hum. Genet. 93:259-264(1994).
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agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                               PDB: 1F5.,

MIM: 253200; -.

R MIM: 272200; -.

R INEAPTO: IPR000917; Sulfatase.

DR PFAM: PF00884; Sulfatase; 1.

DR PROSITE; PS000523; SULFATASE_1: 1.

DR PROSITE; PS00149; SULFATASE_2: 1.

KW Hydrolase; Signal; Glycoprotein; Lysosome; Mucopolysaccharidosis;

KW Disease mutation; Polymorphism; 30 RYLSULFATASE_B.

SIGNAL 37 533 ARYLSULFATASE_B.

''A 1 147 POTEWTIAL.

2-AMINO-3-OXOPROPIONIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                 C -> R (IN MPS-VI; SEVERE FORM).
/FTIG-VAR_007296.
G -> V (IN MPS-VI; INTERMEDIATE FORM).
/FTIG-VAR_007297.
R -> W (IN MPS-VI; INTERMEDIATE FORM).
/FTIG-VAR_007298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R -> Q (IN MPS-VI; INTERMEDIATE FORM).
/FTId=VAR_007299.
Y -> C (IN MPS-VI; MILD/INTERMEDIATE).
                                                                                                                                                                                                                                                                                                                                                                                                            R -> Q (IN MPS-VI; MILD/SEVERE FORM). /FTId=VAR_007295.
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L -> P (IN MPS-VI; MILD FORM).
/FTId=VAR_007301.
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C -> Y (IN MPS-VI; MILD FORM).
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/ -> M (IN REF. 3).
5983FB6911C4789A CRC64;
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/FTId=VAR_007302.
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entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                      EMBL, M32373, AAA51779.1, EMBL, X72735, CAA51272.1, J. BMBL, X72736, CAA51272.1, J. BMBL, X72736, CAA51272.1, JOINED. BMBL, X72738, CAA51272.1, JOINED. BMBL, X72739, CAA51272.1, JOINED. BMBL, X72740, CAA51272.1, JOINED. BMBL, X72741, CAA51272.1, JOINED. BMBL, X72742, CAA51272.1, JOINED. BMBL, X72742, CAA51272.1, JOINED. BMBL, X72742, CAA51272.1, JOINED.
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533 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRALM-ECC 1551 / Oshkosh;
STRALM-ECC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: PHOSPHORYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN
CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN
THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES.
HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H37RV.

MEDLINE-98295987; PubMed-9634230;

MEDLINE-98295987; PubMed-9634230;

MEDLINE-98295987; PubMed-9634230;

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd &

Barres R., Devlin K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Glycosyltransferase; Carbohydrate metabolism; Glycogen metabolism; Pyridoxal phosphate; Complete proteome. BINDING 618 618 KPRIDOXAL PHOSPHATE (BY SIMILARITY). CONFLICT 255 255 K-> E (IN REF. 2).
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-!- CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate {(1,4)-alpha-D-glucosyl}(N-1) + alpha-D-glucose 1-phosphate.-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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E39826B03D5B374F CRC64;
                                                                                                01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
GLGP of Phosphorylase (EC 2.4.1.1).
GLGP OR RV1328 OR MT1370 OR MTCY130.13.
                                        863 AA.
                                        PRT;
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InterPro; IPR000811; Phosphorylase.
PROSITE; PS00102; PHOSPHORYLASE; 1.
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EMBL; AAE007010; AAK45634.1; -.
HSSP; P06738; IXGP.
TIGR; MT1370; -.
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                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 393:537-544(1998).
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                     PHSG_MYCTU
Q10639;
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PHSG_MYCTU
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Gaps

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Score 42; DB 1; Length 533; Pred. No. 17; 0; Mismatches 1; Indels

63.6%; ilarity 85.7%; Conservative 0

Query Match Best Local Similarity Matches 6; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                              Andre C., Dos Santos G., Roulakoff A.;
Andre C., Dos Santos G., Roulakoff A.;
"Cultured neurons from mouse brain reproduce the muscarinic receptor
profile of their tissue of origin.";
Eur. J. Neurosci. 6:1691-1701(1994).
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOLINOSTIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S74908; AAB33576.2; ...
MGD; MGI:88398; Chrm3.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 77m_1; J.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
DOMAIN
                                                                                                                                                                                                                                                                                                                    Gomeza J., Wess J.; Isolation of mouse muscarinic isolation, sequence and functional expression of mouse muscarinic acetylcholine receptor genes."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                               ;
0
                    Score 42; DB 1; Length 863; Pred. No. 25;
                                                Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                        ACM3_MOUSE STANDARD; PRT; 589 AA.
09ER23; 064055;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Muscarinic acetylcholine receptor M3 (Mm3 mAChR).
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                                               0; Mismatches
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MEDLINE=95179320; PubMed=7874308;
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                      Similarity 71.4%; 5; Conservative
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103
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Best Local Similarity
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                         6 (POTENTIAL).

7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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"Molecular cloning of m3 muscarinic acetylcholine receptor in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-87263421; Pubmed-3037705;
Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
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MEDLINE-88077068; PubMed-3120722;
Braun T., Schofield P.R., Shivers B.D., Pritchett D.B., Seeburg
"A novel subtype of muscarinic receptor identified by homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITINE-92037535; PubMed-1657592;
WRESS J., Gdula D., Brann M.R.;
"Site-directed mutagenesis of the m3 muscarinic receptor:
Identification of a series of threonine and tyrosine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
"Cloning and expression of the human and rat m5 muscarinic
acetylcholine receptor genes.";
Neuron 1:403-410(1988).
                                                                                                                                                                                                                                                                                                                                Length 589;
                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                             SIMILARITY.
AB782149EBEE7804 CRC64;
  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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01-AUG-1988 (Rel. 08, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
Muscarinic acetylcholine receptor M3.
                                                                                                                                                                                                                                                                                                                                    Score 41; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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J. Smooth Muscle Res. 34:111-122(1998)
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MEDLINE=99138467; PubMed=9972520;
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MEDLINE=90166521; PubMed=3272174;
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ilarity 71.4%;
Conservative
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Best Local Similarity
' has 5; Conserv?
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                                                                                Wess J., Maggio R., Palmer J.R., Vogel Z.;

"Role of conserved threonine and tyrosine residues in acetylcholine
binding and muscarinic receptor activation. A study with m3
muscarinic receptor point mutants.";

J. Biol. Chem. 267:19313-19319(1992).

-! FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLUIAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIES. & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
Phosphorylation; Multigene EXTRACELLULAR (POTENTIAL).
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(POTENTIAL).

(TYDOLASMIC (POTENTIAL).

(EXTRACELLULAR (POTENTIAL).

(POTENTIAL).

(TOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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involved in agonist but not antagonist binding.";
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                 EMBO J. 10:3729-3734(1991)
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Length 589;

DB 1; 26;

Score 41; Pred. No.

62.1%; 71.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sui A.-L., Chou W.-Y., Kao L.-S.;
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIES, MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
     Gaps
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-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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GCRDb; GCR_1227; --
GCRDb; GCR_1227; --
GCRDb; GCR_1227; --
InterPro: IPR000276; GPCR_Rhodpsn.
PROSTIE: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSTIE: P550262; G_PROTEIN_RECEP_FI_1; 1.
PROSTIE: P550262; G_PROTEIN_RECEP_FI_2; 1.
PROSTIE: P55027; G_PROTEIN_RECEP_FI_2; 1.
PROSTIE: P550262; G_PROTEIN_RECEP_FI_2; 1.
PS50262; G_PROTEIN_RECEP_FI_2; 1.
PS50262; G_PROTEIN_RECEP_FI_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Sukaryota, Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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"cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 receptor.";
     Indels
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5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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01-NoV-1995 (Rel. 32, Last sequence update)
11-NUV-1998 (Rel. 36, Last annotation update)
Muscarinic acetylcholine receptor M3.
Mismatches
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MEDLINE=94339178; PubMed=8061048;
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Conservative
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                                                                            524 YWNLGYW 530
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P41984;
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Local Similarity 71.4
hes 5; Conservative
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             Mycoplasma pneumoniae.
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Hypothetical prot
MPN335 OR MP501.
Phosphorylation;
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ID YD35_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENTARE CYCLASE, BREAKDOWN OF PHOSPHOTNOSTYIDES & MODULATION OF POTASSIUM CHANNELS THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88296835; PubMed=3402600;
Akiba I., Kubo T., Maeda A., Bujo H., Nakai J., Mishina M., Numa S.;
"Primary structure of porcine muscarinic acetylcholine receptor III
and antagonist binding studies.";
FEBS Lett. 235:257-261(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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GCRDb; GCR_0104; -.
InterPro; IPR00025; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRRHONOPSN.
PRINTS; PR00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                            (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                                               (POTENTIAL)
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                                                                                                                                                                                                                                                                                                              Length 590;
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                           CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTINIED (GLCNAC. . ) (ELCNAC. . )
EXTRACELLULAR (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last annotation update)
Muscarinic acetylcholine receptor M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 AA.
                                                                                                                                                                                                                                                                                                              Score 41; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                               ₹.
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                                                                                                                                                                                                                                                                                                              62.1%;
71.4%;
                                                                                                                                                                                                                                                               66103
                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                              15
41
48
53
221
424
                                                                                                                                                                                                              452
461
467
590 AA;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           525 YWNLGYW 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                           2 ywgcgyw 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACM3_PIG
ID ACM3_PIG
AC P11483;
                                                                                                                                             DISULFID
CONFLICT
CONFLICT
CONFLICT
                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                CONFLICT
                                                 CARBOHYD
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   DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.PNEUMONIAE MPN333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Multigene family, G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.1%; Score 41; DB 1; Length 590; 71.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR000188; GABAA_receptor.
Pfam, PF02932; Neur_chan_memb; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                             4 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
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                                                                                                                     2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                         (POTENTIAL)
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01-NoV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Hypothetical protein MPN335 (F10_orf741).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         741 AA
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                                                             (POTENTIAL)
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                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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AC 092740; 092739; p78541; p78558;
DT 01-ARP-1988 (Rel. 07, Created)
DT 01-ARP-1980 (Rel. 14, Last sequence update)
DT 01-ARP-1090 (Rel. 41, Last annotation update)
DT 01-ARP-1090 (Rel. 41, Last annotation update)
DF Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebrosside Sulfate activator) (CSAC) (Dispersin) (sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase) (E (Protein C) (Component C)].
B (Protein C) (Component C)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rorman E.G., Grabowski G.A.; "Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sphingolipid hydrolase activator proteins are encoded by single genes in humans and rats."; Genomics 5:486-492(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
MEDLINE-89255151; PubMed=2498298;
Nakano T., Sandhoff K., Stuemper J., Christomanou H., Suzuki K.;
"Structure of full-length cDNA coding for sulfatide activator, a
Co-beta-glucosidase and two other homologous proteins: two alternate forms of the sulfatide activator.";
J. Biochem. 105:152-154(1989).
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saposin A (Protein A);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The organization of the gene for the human cerebroside sulfate
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                                                                                                                                                                                                                                                                       Length 741;
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                                                                                                                                                                  POTENTIAL.
1776A96BCF83567F CRC64;
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                                                                                                                                                                                                                                                                       DB 31;
                                                                                                                                                                                                                                                                       Score 41; DB Pred. No. 31; 0; Mismatches
  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
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MEDLINE-88068647; PubMed=2825202;
Dewji N.N., Wenger D.A., O'Brien J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90129043; PubMed=2515150;
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                                                                                                                                                                                            MW.
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                                                                                                                                                                                                                                                                     62.1%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                   85025
  54
96
140
176
207
675
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Strausberg R.;
                                                                                                                                                                                      741 AA;
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                   TRANSMEM
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                     Query Match
                                                  TRANSMEM
                                                                                 TRANSMEM
                                                                                                       TRANSMEM
                            TRANSMEM
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SAP_HUMAN
AC P07602,
AC P02740,
AC P07602,
AC P02740,
AC P07602,
AC
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FT
FT
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Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J., Waring A.J., To T., Fluharty C.B., Faull K.F.; "Preparation of the cerebroside sulfate activator (CSAct or saposin B)
                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Kidney;
MEDLINE-91006165; PubMed-2209618;
Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;
"The complete amino-acid sequences of human ganglioside GM2 activator protein and cerebroside sulfate activator protein.";
Eur. J. Biochem. 192:709-714(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89207118; PubMed-3242555; Kleinschmidt T., Christomanou H., Braunitzer G.; "Complete amino-acid sequence of the naturally occurring A2 activator soulferin for enzymic sphingomyelin degradation: identity to the sulfatide activator protein (SAP-1)."; Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQÜENCE OF 311-390.

MEDLINE-88163077; Pubbed=3442600;

RELINE-88163077; Pubbed=3442600;

"Complete amino-acid sequence and carbohydrate content of the naturally occurring glucosyleeramide activator protein (Al activator) absent from a new human Gaucher disease variant.";

Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
Nucleotide sequence of cloned cDNA for human sphingolipid activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89000190; PubMed=3048308;
Furst W., Machleidt W., Sandhoff K.;
"The precursor of sulfatide activator protein is processed to three
                                                                                                                                                                                                                                                           Hill F., O'Brien J.S.; "Molecular cloning of the sphingolipid activator protein-1 (SAP-1), the sulfatide sulfatase activator.";
                                                                                                           Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kondoh K., Hineno T., Sano A., Kakimoto Y.;
"Isolation and characterization of prosaposin from human milk.";
Blochem. Blophys. Res. Commun. 181:286-292(1991).
                                                                                                                                                                                                                                          Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE OF SAPOSIN B, AND STRUCTURE OF CARBOHYDRATES
                                                                                                                                              "Saposin A: second cerebrosidase activator protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89025876; PubMed-2845979;
Morlinoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;
Mosposin D: a sphingomyelinase activator.";
Blochem. Biophys. Res. Commun. 156:403-410(1988).
                 protein 1 precursor.";
Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).
                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 134:989-994(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. Hoppe-Seyler 369:317-328(1988).
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STRUCTURE OF CARBOHYDRATE ON ASN-215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human urine.";
Genet. Metab. 68:391-403(1999).
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                                                                                                                                                                                                   SEQUENCE OF 195-263 FROM N.A. MEDLINE=86130593; PubMed=2868718;
                                                                                           PubMed=2717620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92068206; PubMed=1958198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE OF 405-484
                                                                        SEQUENCE OF 60-142.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 195-274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from human urine.
                                                                                                                              Kishimoto Y.;
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                                                                        PARTIAL
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MASS

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-!- SUBCELLULAR LOCATION: Lysosomal.
-!- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),
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                                                                                                        60.6%;
62.5%;
                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 312-391.
                                                                                                                                                   Best Local Similarity
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                                                                                                            Query Match
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-!- FUNCTION: The lysosomal degradation of sphingolipids takes place by the sequential action of specific hydrolases. Some of these enzymes require specific low-molecular mass, non-enzymic proteins: the sphingolipids activator proteins (coprofeins).

-!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of glucosylceramide by beta-glucosylceramides (EC 3.2.1.45) and galactosylceramide by beta-glacosylceramidase (EC 3.2.1.46). Saposin C apparently acts by combining with the enzyme and acidic lipid to form an activated complex, rather than by solubilizing
                               Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P., Stevens R.L., Fluharty A.L., Eluharty A.L., Eluharty A.L., Structure of the asparaqine-linked sugar chains of porcine kidney and human urine cerebroside sulfate activator protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91285107; PubMed=2060627;
Schnabel D., Schroeder M., Sandhoff K.;
"Mutation in the sphingolipid activator protein 2 in a patient with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Saposin B stimulates the hydrolysis of galacto-cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1 agaqliosides by beta-galactosidase (EC 3.2.1.23) and globotriacyslearmide by alpha galactosidase A (EC 3.2.1.22). Saposin B forms a solubilizing complex with the substrates of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase activator (EC 3.1.4.12).
                                                                                                                                                                                                                                                                                                                  MEDILINE—99441404; PubMed=10510427;
Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,
Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,
"Cerbinsty C.B., Fluharty A.L.;
"Cerebroside sulfate activator protein (Saposin B): chromatographic
and electrospray mass spectrometric properties.";
J. Mass Spectrom. 34:1040-1054(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90147748; PubMed=2302219; Menger D.A.; Zhang X.-L., Degala G., Wenger D.A.; Phong X.-L., Degala G., Wenger D.A.; Protection of a point mutation in sphingolipid activator protein-1 mRNA in patlents with a variant form of metachromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,
O'Brien J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALFERNATIVE SPLICING.
MEDLINE=91210267; PubMed=2019586;
Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95170731; PubMed=7866401; Gleselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.; "Molecular genetics of metachromatic leukodystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sulfatide activator protein. Alternative splicing that generates three mRNAs and a newly found mutation responsible for a clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Д
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Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 166:1017-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Saposin B is a homodimer.
                                                                                                                                                                                  J. Mass Spectrom. 35:1416-1424(2000).
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MEDLINE=21110404; PubMed=11180632;
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FEBS Lett. 284:57-59(1991).
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Suzuki K.

disease.

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MEDLINE-92207994. PubMed-1554743;

MOTITAR N. Maruno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,

A Morita N.; Maruno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,

Morita N.; from bovine spleen; complete amino acid sequence and

"Saposin-C from bovine spleen; complete amino acid sequence and

relation between the structure and its biological activity.";

Blochim. Biophys. Acta 1120:75-80(1992).

LIEUDATION: THE LYSOCAMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE

BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE

BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE

BY THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROPERINS) (BY SIMILARITY).

C. INDRING SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF

GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND

C. ALACTOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND

C. SAPOSIN-C APPAREMILY ACTS BY COMBINING WITH THE BRYTHE AND ACIDIC

LIPPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEREBROSIDE SULPATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
CEREBROSIDES SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND
GLOBOTRIAOSYLCERANIDE BY ALPHA-CALACTOSIDASE A (EC 3.2.1.22),
SAPOSIN B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
STHINGOLIPID HYDROLASES (BY SIMILARITY).
FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE
ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                 Databourn Standard, Fri, 525 Ac. (198264; 098264; 01-805. Rel. 23, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (CSACT) (Dispersin) (SAP-1) (Cerebroside sulfate activator) (Sphingolipid activator protein 1) (SAP-1) (Cerebroside activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                               ö
Length 524;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Mammary gland;
Azuma N., Yoshida K.;
"RT-PCR cloning of bovine prosaposin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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-!- SIMÍLARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
-!- SIMÍLARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
  Score 40; DB 1;
                                                                                                                                                                                                                                                                    525 AA.
                                               0; Mismatches
                           Pred. No.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003119; SapA.
InterPro; IPR003119; SapA.
InterPro; IPR003119; SapB.
InterPro; IPR000119; SapB.
InterPro; IPR000129; SapB.
Pfam; PF02199; SapA; 2.
Probom; PD012321; SapBs; 3.
Probom; PD012321; SapBs; 3.
SWART; SM00162; SAPA; 2.
SWART; SM00118; SAPB; 4.
Sulfation; Signal; Glycoprotein; Re SIGNAL
                                                                                     MEDLINE=92272718; PubMed=1590788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S36200; AAB22175.1; -. EMBL; S71616; AAB31059.1; -. EMBL; U27340; AAA92567.1; -. EMBL; U57999; AAB02695.1; -.
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                                                            SEQUENCE FROM N.A.
                      Mammalla; Eutheri
NCBI_TaxID=10090;
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                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SAPOSIN C.
SAPOSIN L.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 3.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 7.
BY SIMILARITY.
BY 
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061207; 064219; 064006; 060861;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Sulfated 91ycoprotein 1 precursor (SGP-1) (Prosaposin).
PSAP OR SGP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> Q (IN REF. 2).
-> S (IN REF. 1).
293AFCOFB9C4FA99 CRC64;
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MQPK ->
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PIR; S21770; S21770.
InterPro; IPR003119; SapA.
InterPro; IPR003004; SapB.
InterPro; IPR003299; Saposin.
Pfam; PF02199; SAPA; 2.
ProDom; PD001732; SapB; 3.
ProDom; PD012321; Saposin; 1.
SMART; SM00162; SAPA; 2.
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Best Local Similarity 62.5
Matches 5; Conservative
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SIGNAL 1 16
CHAIN 60 142
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Mus musculus (Mouse).
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367
525 AA;
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DD SAP_MOUSE
DT 15-DEC
DT 15-DEC
DT 16-OCT
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                                                                                                   SEQUENCE FROM N.A.
MEDLINE-9421317; PubMed-8003952;
Sprecher-Levy H., Orr-Urtreger A., Lonai P., Horowitz M.;
"Muxine prosaposin: expression in the reproductive system of a gene implicated in human genetic disease.";
Cell. Mol. Biol. 40:233-233(1994).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-96084310; Pubmed-8565332;
Cao Q.P., Crain W.R.,
"Expression of SGP-1 mRNA in preimplantation mouse embryos.";
Dev. Genet. 17:263-271(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
STRAIN-BALB/C; Hay N.N., Morales C.R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLILAR LOCATION: Extracellular.
-!- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
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BY SIMILARITY.
SULFATED GIXCOROTEIN 1.
SAPOSIN-LIKE TYPE A 1.
SAPOSIN-LIKE TYPE B 1.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 2.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE B 4.
SAPOSIN-LIKE TYPE A 2.
BY SIMILARITY.
Tsuda M., Sakiyama T., Endo H., Kitagawa T.,
"The primary structure of mouse saposin.";
Biochem. Biophys. Res. Commun. 184:1266-1272(1992).
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STRAIN=IMI 206040;
MEDLINE=95291429; PubMed=7773384;
Vasseur V.V., van Montagu M.M., Goldman G.G.H.;
"Trichoderma hazzianum genes induced during growth on Rhizoctonia solani cell walls.";
                         (POTENTIAL).
(POTENTIAL).
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    (POTENTIAL).
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Hypocreales; mitosporic Hypocreales; Trichoderma.
NCBL_TaxID=5544;
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- SUBCELULAR LOCATION: Integral membrane protein.
-!- INDGTION: DURING MYCOPARASITISM.
-!- INDGTION: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 557;
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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N-LINKED (GLCNAC...)
N-SINKER. 2).
MS -> SA (IN REF. 2).
MS -> SA (IN REF. 2).
MS -> SA (IN REF. 2).
MS -> CIN REF. 2).
MSSING (IN REF. 3).
MSSING (IN REF. 4).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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Interpro; IPR002293; AA_rel_permease_1.
Interpro; IPR002027; Amino_acid_permease.
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62.5%;
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Pfam; PF00324; aa_permeases; 1.
PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
Transport; Amino-acid transport; Transmembrane.
92
                                                                                                                                                                                            Score 40; DB 1;
Pred. No. 35;
0; Mismatches
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ilarity 71.48;
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099VNF1 095462 095753 095753 096753 097050 095070 095070 091770 091770 091770 091771 091771 09209 092177 09220 09220 09220 09220 09220 09220 09220 09220

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ALIGNMENTS

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                                                      August 12, 2002, 17:28:14; Search time 41.64 Seconds (without alignments) 33.236 Million cell updates/sec
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                                                                                                                                                                         562222
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries

    protein search, using sw model

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3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate:*
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MEDLINE=20351236; PubMed=10891382;
MEDLINE=20351236; PubMed=10891382;
MEDLINE=20351236; PubMed=10891382;
MEDLINE=20351236; PubMed=10891382;
De Micco P., de Lamballerie X.;
De Micco P., de Lamballerie X.;
Sequence Determination and Analysis of the Full-Length Genome of Colorado Tick Fever Virus, the Type Species of Genus Coltivirus (Family Reoviridae).";
Biochem. Biophys. Res. Commun. 273:1121-1125(2000).
EMBL; AF139759; AAG00068.1; -.
SEQUENCE 1182 AA; 135011 MW; E1F5F3515E9204C9 CRC64; ö 12; Length 1182; Indels Created)
Last sequence update)
Last annotation update) Colorado tick fever virus. Viruses; dsRNA viruses; Recviridae; Coltivirus. NCBI\_TaxID=46839; DB 28; PRT; 1182 AA 269 AA 72.7%; Score 48; DB 100.0%; Pred. No. 28; ive 0; Mismatches PRT; Q9ENL3; 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, 6; Conservative PRELIMINARY; PRELIMINARY; Query Match Best Local Similarity Matches 6; Conserv [1] SEQUENCE FROM N.A. 480 CYWGCG 485 9 1 cywgcg ( 9x6260 7 RESULT 09C9X6 δ g HA H

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Q9C9X6; 01-JUN-2001 (TrEMBLrel. 17, Created)

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Q9ENL3 Q9C9X6 Q9LDE2 Q9SUDE2 Q9SUD19 Q9D929 Q9D929 Q99675 Q99675 Q96BX2 P97587

722 6688.9 6633.6 6633.

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   STRAIN—CV. COLUMEN;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MUTHCE O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Muthce O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Annurer J.L., Jenkins J., Hansen N.F., Hughes B., Hulzar L.,

Annurer J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Annurer J.L., Aremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Neoney T., Rowley B.,

Rakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tambunga G., Toriumi M.J., Town C.D.,

Wu Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0EC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
11-0BC-2001 (TrEMBLrel. 19, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R., "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 16;
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 408:816-820(2000).
EMBL, AC012563; AA632002.1; -.
Hypothetical protein.
SEQUENCE 269 AA; 30392 MW; 2753AB3AD6063FE8 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                    NCBI_TaxID=3702;
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SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Kon L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Chiou J., Choi E., Conn D., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
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Arabidopsis thaliana (Mouse-ear cress).
Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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STRAIN-CV. COLUMBIA.
MEDLINE-20083487; PubMed-10617197;
ALIN X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Mawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Pamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AC006917; AAF79219.1; -. EMBL; AC010657; AAF63172.1; -. EMBL; AY058073; AAF4311.1; -. SEQUENCE 279 AA; 31168 MW; BAB996037E04D372 CRC64;
Ecker J.R.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C., K., Squence and analysis of chromosome 2 of the plant Arabidopsis thallana."
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-93003385; Pubmed-1390929; Kobayashi T., Makita A.; Kobayashi T., Honke K., Jin T., Gasa S., Miyazaki T., Makita A.; Components and proteolytic processing sites of arylsulfatase B from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006532; AAF18588.1; -.
SEQUENCE 283 AA; 31648 MW; BAFBFCBD92262E07 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                       Score 45.5; DB 10;
Pred. No. 17;
0; Mismatches 1;
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Biochim. Biophys. Acta 1159:243-247(1992).
HSSP; P15848; 1FSU.
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01-MAY-2000 (TTEMBLrel. 13, Last sequence
01-CCT-2000 (TTEMBLrel. 15, Last annotation
ARYLSULFATASE B (EC 3.1.6.1) (FRAGMENTS).
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77.88;
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7270 MW;
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85.78;
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                                                                                                                                     Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                       Query Match 68.9
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 CYRWGCGGW 212
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SEQUENCE
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A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Itaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Alio T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito T., Ashburner M., Batalov S., Casavant T., Ridota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Saubli F., Suzuki R., Tomite M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Bronstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M., Bonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Mashiwa-Bonis A., Kawaji H., Kohtsuki S., A., Wassing Y., Kawaji H., Kohtsuki S.,
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Appel S., Bergheim A., Reichwald K., Reis A., Rosenthal A., Ramsay M.,
Hennies H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Transcript map of the KWE critical region on chromosome 8p22-p23."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ301560; CAC82736.1; - Hypothetical protein.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). EMBL; AK007402; BAB25015.1; -. MGD; MGI:1916368; IBI0009H17Rik. SEQUENCE 212 AA; 24313 MW; 7D5EDF67496F61C4 CRC64;
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Last annotation update)
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100.0%; Pred. No. 56;
iive 0; Mismatches
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100.0%; Pred. No. 42.
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                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; PubMed-11217851;
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(TrEMBLrel. 19, I
(TrEMBLrel. 19, I
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
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01-DEC-2001
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SEQUENCE
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                               Madden S.L., Galella E.A., Riley D., Bertelsen A.H., Beaudry G.A.; Tinduction of cell growth regulatory genes by p53."; Cancer Res. 56:5384-5990(1996).

EMBL; U66471; AAC52951.1; ...
EMBL; U66471; AAC52951.1; ...
SMART; SMO01841; Znf_ring.
SMART; SMO0184; RIG; T_ring.
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                                                                                                                                                                                                                                                                                                                             63.6%; Score 42; DB 11; Length 332; 100.0%; Pred. No. 64; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BRISTOL N2;
Geisel C., Wamsley P.;
"The sequence of C. elegans cosmid C07G3.";
submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AROIG432, ARB65382.1; -.
InterPro; IPR003002; 7TM_chemorecept_1.
InterPro; IPR000168; 7TM_nematode.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 38.5 KDA PROTEIN.
O1-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL GROWTH REGULATOR RCGR19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                SEQUENCE FROM N.A.
STRAIN-FISHER; TISSUE-FIBROBLAST;
MEDLINE-97122496; PubMed-8968090;
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342 AA; 38469 MW;
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Best Local Similarity luv...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01461; 7tm_4; 1. Hypothetical protein. SEQUENCE 342 AA: 3RAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                 NCBI_TaxID=10116;
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98 CYWGC 102
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC015063; AAH15063.1; -. SEQUENCE 332 AA; 38268 MW; OFECCCE1E87950FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA; 38241 MW; 2F1FC0D12B710C80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
CELL GROWTH REGGLATORY WITH RING FINGER DOWAIN.
                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CELL GROWTH REGULATOR CGR19.
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                                                 PRT;
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                   Homo sapiens (Human).
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98 CYWGC 102
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Q96BX2;
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MEDINE-95241511; Pubmed-7724574; Simons J.N., Pilot-Matias T.J., Leary T.P., Dawson G.J., Desai S.M., Schlauder G.G., Muerhoff A.S., Erker J.C., Buljk S.L., Chalmers M.L., Van Sant C.L., Mushahwar I.K.; "Identification of two flavivirus-like genomes in the GB hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SEQUENCE FROM N.A.
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SEQUENCE FROM S.M., Schultz D.E., Lemon S.M., Mushahwar I.K.;
SIMONS J.N., Desal S.M., Schultz D.E., Lemon S.M., Mushahwar I.K.;
"Translation initiation in GB viruses A and C: evidence for internal
Translation initiation in GB viruses A and C: evidence for internal
J. Virol. 70:6126:6135(1996).
EMBL; U22303, AAC55983.1; -..
MESSP, P27958; IHEI.
MEROPS; S29.002; -..
MEROPS; U39.001; -..
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Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Geisel C., Wamsley P.;
"The sequence of C. elegans cosmid C07G3.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF016432, AAB65377.1;
InterPro; IPR003002, 77M_chemorecept_1.
InterPro; IPR00168; 77M_nematode.
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 92:3401-3405(1995).
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100.0%; Pred. No. 67;
iive 0; Mismatches
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[1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
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HCV_NS3.
HCV_NS4a.
HCV_NS4b.
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InterPro; IPR002518;
InterPro; IPR004109;
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InterPro; IPR001490;
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Matches 5; Conserv
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Q96898
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016432; ABA65378.1;
InterPro; IPR003002; 7TM_chemorecept_1.
InterPro; IPR00168; 7TM_nematode.
InterPro; IPR00154; HTH_GatR.
InterPro; IPR001307; Rhodanese.
Figur, PF0161; 7tm_4; 1.
PROSITE; PS00043; HTH_GNTR_FAMILY; UNKNOWN_1.
PROSITE; PS00080; RHODANESE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRIGIOL N2;
Geisel C., Wamsley P.;
"The sequence of C. elegans cosmid C07G3.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .l protein.
347 AA; 38948 MW; BOBCF0891EB6AF57 CRC64;
                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 38.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 39.4 KDA PROTEIN.
                                                                                                                                                                                                                                 347 AA.
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MEDLINE-99069613; PubMed-9851916;
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Best Local Similarity 100.
Matches 5; Conservative
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                                                    97 CYWGC 101
                  1 cywgc 5
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SEQUENCE 34
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016323
AC 016323
AC 016323
DT 01-JAN
DT 01-JAN
DT 01-DEC
DE HYPOTH
OS CACHOTH

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MEDITRE-97126113; PubMed-8971037;
Leary T.P., Desai S.M., Yamaguchi J., Chalmers M.L., Schlauder G.G.,
Dawson G.J., Mushahwar I.K.;
"Species-specific variants of GB virus A in captive monkeys.";
J. Virol. 70:9028-9030(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae.
NCBI_TaxID=39112;
                     InterPro; IPR002166; HCV_RGRP.
InterPro; IPR002166; HCV_RGRP.
InterPro; IPR003880; Phosphopant_attach.
Pfam; PF01539; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4; 1.
Pfam; PF01006; HCV_NS54; 1.
Pfam; PF01001; HCV_NS54; 1.
Pfam; PF01009; HCV_RGRP; 1.
Pfam; PF01998; HCV_RGRP; 1.
PR05ITS; PS00012; PH0SPHOPANTETHEINE; UNKNOWN_1.
NONSITUCINEL DIOCIAI; POLYPROPER; PA0735FCZED283B1 CRC64; SEQUENCE 2954 AA; 318833 MW; 4A0C335FCZED283B1 CRC64;
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MEDLINE-97437486; PubMed=9292019;
MEDLINE-97437486; PubMed=9292019;
Leary T.P., Desai S.M., Erker J.C., Mushahwar I.K.;
"The sequence and genomic organization of a GB virus A variant isolated from captive tamarins.";
J. Gen. Virol. 78:0-0(0).
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94421; AAB71133.1; -.
HSSP; P27958; IHEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             041892 PRELIMINARY; PRT; 2967 AA.
041892;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOME POLYPROTEIN.
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Interpro; IPR002518; HCV_NS2.
Interpro; IPR0004109; HCV_NS3.
Interpro; IPR0001409; HCV_NS4a.
Interpro; IPR0001490; HCV_NS4b.
Interpro; IPR001808; HCV_NS5a.
Interpro; IPR002166; HCV_NS5a.
Interpro; IPR002166; HCV_RGRP.
Interpro; IPR000165; Myb_DNa_bind.
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Pfam; PF02807; HCV_NS3; 1.
Pfam; PF01006; HCV_NS45; 1.
Pfam; PF01001; HCV_NS45; 1.
Pfam; PF01506; HCV_NS45; 1.
Pfam; PF01506; HCV_NS45; 1.
Pfam; PF01509; HCV_NS4P; 1.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
InterPro; IPR002868; HCV_NS5a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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277 CQWGSAYW 284
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DR PROSITE; PS00037; MYB_1; UNKNOWN_1.

KW Nonstructural protein; Polyprotein; RNA-directed RNA polymerase.

SQ SEQUENCE 2967 AA; 321140 MW; 9AAB97B830C5D199 CRC64;

Query Match

Best Local Similarity 62.3%; Score 42; DB 12; Length 2967;

Best Local Similarity 62.3%; Pred. No. 5e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 cywgcgyw 8

| | | | | | | | |
| Db 277 CQWGSAYW 284

Search completed: August 12, 2002, 17:28:16
Job time: 363 sec
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August 12, 2002, 17:21:41; Search time 51.76 Seconds (without alignments) 17.168 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                           747574
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    747574 seqs, 111073796 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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66
                                                                                                                                                                                                                          1 cywgcgyw 8
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A\_Geneseq\_032802:\*

| SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
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| SIDSJ/gcgdata/hold-geneseq/geneseqp-embl/AA3399.DAT:\*
| SIDSJ/gcgdata/h

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Fluorine-18 (F-18)	Immunogenic peptid	Telomerase associa	H2 homologue of pr	Arabidopsis thalia		Arabidopsis thalia				
SUMMARIES	OI		AAY76817	AAY66023	AAB18511	AAG40353	AAG60115	AAG05644	AAG38268	AAG40352	AAG60114	AAG05643
	DB	20	21	21	21	21	21	21	21	21	21	21
	Query Match Length DB	80	œ	54	841	233	238	252	252	252	257	279
æ	Query Match	100.0	100.0	72.7	71.2	68.8	68.9	68.9	68.8	68.8	68.8	68.8
	Score	99	99	48	47	45.5	45.5	45.5	45.5	45.5	45.5	45.5
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ល ល ល ល ល ល	Fluorine-18 (F-18) Immunogenic peptid Human polypeptide Human nervous syst Somatostatin deriv Human ORFX ORF2480	Human cell growth Rat cell growth re A human cell growt Human colon cancer Human sulfatase pr Hepatitis GB virus	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Drosophila melanog Muscarinic M3 rece Human protein sequ Novel human diagno Human activated T- FCTR4. Homo sapie Somatostatin deriv Propionibacterium Arabidopsis thalia
AAG3826 AAG4035 AAG3826 AAG6011 AAG0564	0 AAY03716 1 AAY76816 2 AA010292 2 ABB16263 0 AAY42908 1 AAB42716		AAR9434 ABB4132 AAM6219 AAM7499 AAM3511 AAM6509 AAM6509	ABB69676 AAP90553 AAP90553 AABC02902 AAU00023 AAB47327 AAU39355 AAU39355
	8 7 7 1 1 1 1 1		163 32 32 32 32 76	126 22 358 10 441 22 602 22 1851 22 1604 22 7 20 105 22 125 21
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13 14 11 17 17	118 22 23	00000000000000000000000000000000000000	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	338 338 445 444 55

## ALIGNMENTS

XX AAY03715; XX AAY03715; XX AAY03715; XX AAY03715; XX B Fluorine-18 (F-18) labeled peptide 2. XX XX B Fluorine-18 (F-18) labeled peptide 2. XX I8F radionuclide; targeting vector; positron emission tomography; F-18; XX XX Synthetic. XX KW Key I Location/Qualifiers FT Misc-difference 1 Anote= "N-terminal acetylation; optionally has a free or protected thiol group" FT Misc-difference 3 FT Misc-difference 3 FT Misc-difference 3 FT Misc-difference 5 FT Misc-difference 7 FT Misc-difference 7 FT Misc-difference 8 FT Misc-difference 7 FT Misc-difference 8
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(first entry)
                                                                                                                                                                                                                                                                                                              Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                   (IMMU-) IMMUNOMEDICS INC.
/note=
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                                                                                       'note=
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Best Local Similarity
                                                                       Misc-difference 7
                                                                                                   Misc-difference 8
              Misc-difference 5
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Synthetic.
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14-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                          conjugates
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                                                                                                                                                                                                                                  into peptide-containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with cliuorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CRIR2-(CH2)m-K, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bears at least one leaving group comprising 1, Br, Cl. x azide, tosylate, mesylate, nosylate or tiflate, n, m = 0-2, n+m = 0-2, coptionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I, Br, Cl. azide, tosylate, mesylate, triflate, H, COMH2, COOH, CH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl coptionally substituted by COMH2, COOH, OH, sulfonic acid, tertiary amine or quaternary ammonium, alkyl coptionally substituted by COMH2, COOH, OH, sulfonic acid, tertiary amine or quaternary ammonium, alkyl or phenyl. The method is used for Radiolabeling peptide-containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "acetylated; modified with free amino acid group,
   protected amino acid group, chelating agent or a
   metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                              targeting vectors such as proteins, antibodies, antibody fragments and receptor targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY03714-716 represent examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
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                                                                                                                                                                                                                          The invention relates to a method for incorporating 18F radionuclide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
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                                                                                                                                                                Radiolabeling thiol-containing peptides with fluorine-18
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100.0%; Pred. No. 6.4e+05;
ive 0; Mismatches 0;
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Misc-difference 3
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                                                                                                                                                                                            Claim 14; Page 15; 22pp; English.
               98WO-US18268
                                           97US-0057485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                         (IMMU-) IMMUNOMEDICS INC
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Matches 8; Conserv
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Misc-difference
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              03-SEP-1998;
                                                                                                     Griffiths GL,
                                          03-SEP-1997;
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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating a bi-specific diseased tissues in a patient comprising administring a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds cargetable conjugate. The methods and bi-specific antibodies and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
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                                                                  'D-form residue; modified with free amino acid
group, protected amino acid group, chelating
agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bi-specific antibodies that bind specific target tissue and targeted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McBride WJ,
                                                                      "D-form residue;
"D-form residue"
                                                                                                                                                                                                                                                                                                      /note= "D-form residue"
                                                                                                                                                                                                                           "D-form residue"
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The present sequence represents a H2 homologue of a prolyl tripeptidyl-peptidase (designated DPP) from Porphyromonas gingivalis. The prolyl tripeptidyl-peptidase has an amidolythic activity, and cleaves a peptide bond in a target polypeptide having at least 4 amino acids. This bond is between a proline and an amino acid attached to the This bond is between a proline and an amino acid attached to the Japha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodonal disease such as ginglvitis and periodontitis caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                              Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful for identifying its inhibitor which is useful for protecting an animal from a periodontal disease such as gingivitis and periodontitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 21; Length 84
Pred. No. 1.5e+02;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 50058.
                                                                                                                                                (UYGE-) UNIV GEORGIA RES FOUND INC.
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990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
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                                                             03-MAR-2000; 2000WO-US05551
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                                                                                                                                                                                                                                                                                                       WPI; 2000-594181/56
                                                                                                                                                                    TRAVIS J. POTEMPA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                  BANB/) BANBULA A.
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25-MAR-1999;
29-MAR-1999;
                    08-SEP-2000
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(iii) comprise 0-10 amino acid from the carboxyl terminus of the normal part of the protein sequence preceding the amino terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant sequence and may further extend to the carboxyl terminus of the mutant part of the protein as determined by a new stop codon generated by the frameshiff mutation; and antigen presenting cell (APC), T cell response.

The genes that the peptides are derived from, are characterised as autigen presenting cell (APC), T cell response.

The genes that the peptides are derived from, are characterised as succeptible to frameshiff mutation by having a mono nucleoside base repeat sequence of at least 5 residues, or a di-nucleoside base residues corrected by the addition or deletion of 1 or 2 nucleoside base residues from the repeat sequence. The novel peptides can elicit T cell responses and toxicity against tumours and cancer cells carrying genes with cameshift mutations. The novel peptides and DNA sequences can be used concerned.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides AAV55684-Y66142 are fragments of mutant proteins arising from a frameshift mutation in a gene from a cancer cell. The peptides are characterised in that they:

(i) are at least 8 amino acids long and a fragment of a mutant protein arising from a frameshift mutation in a gene of a cancer cell; arising from a frameshift mutation in a gene of a cancer cell; (i) consists of at least one amino acid of the mutant part of a protein consists of a cancer cell.
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gingivitis; periodontitis.
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                                                                                                                                                                                                                                                                                                                  New peptides derived from genes with frameshift mutations, used to develop products for the treatment and prophylaxis of cancers
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PR 20-JUL-1999; 99US-0144352.
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PR 21-JUL-1999; 99US-0146088.
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PR 23-JUC-1999; 99US-014918.
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PR 23-JUC-1999; 99US-0155059.
PR 23-SEP-1999; 99US-0155059.
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Pred. No. 80;
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ilarity 77.8%;
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Pred. No. 82;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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05-MAR-1999;
09-MAR-1999;
23-SEP-1999;
24-SEP-1999;
25-SEP-1999;
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15-0CT-1999;
16-0CT-1999;
17-0CT-1999;
18-0CT-1999;
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                      US-08-445-586-10
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                                                                                                 August 12, 2002, 17:22:10; Search time 21.42 Seconds (Without alignments) 9.123 Million cell updates/sec
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Sequence 191,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-484-494-13
US-08-410-247-2
US-08-100-247-2
US-08-232-513A-3
US-08-484-594A-2
US-08-484-126-1
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US-08-905-223-452
US-08-601-435-2
US-08-931-047-2
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US-08-943-956A-2
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence:
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28 34 51.5 13 4 US-09-042-107-112 Sequence 112, App 29 34 51.5 13 4 US-09-042-107-191 Sequence 191, App 31 34 51.5 13 4 US-09-042-107-191 Sequence 191, App 31 34 51.5 2 US-08-761-248B-2 Sequence 7, Appli 32 34 51.5 212 US-08-761-248B-6 Sequence 6, Appli 34 51.5 220 2 US-08-761-248B-6 Sequence 6, Appli 35 34 51.5 220 2 US-08-18-2190-3 Sequence 12, Appli 36 34 51.5 333 1 US-08-118-270-12 Sequence 12, Appli 37 34 51.5 333 5 PCT-US93-08528-12 Sequence 12, Appli 38 31 US-08-608-241-2 Sequence 2, Appli 39 34 51.5 376 1 US-08-919-953-2 Sequence 2, Appli 40 34 51.5 376 2 US-08-919-953-2 Sequence 2, Appli 41 34 51.5 4 US-09-192-993-1 Sequence 2, Appli 42 34 51.5 726 4 US-09-992-11 Sequence 11, Appli 42 34 51.5 726 4 US-09-912-2911 Sequence 11, Appli 43 51.5 726 4 US-09-302-812-10 Sequence 10, Appli 44 34 51.5 726 4 US-09-312-10 Sequence 10, Appli 45 31 50.0 11 US-08-612-10 Sequence 10, Appli 45 33 50.0 11 US-08-512-10 Sequence 339, Appli 45 339, App
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ALIGNMENTS

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RESULT 16.00 15.586-10 15.08445586

Sequence 10, Application US/08445586

Patent No. 5627050

GENERAL INFORMATION: Toshimi
APPLICANT: Tro, Toshimi
APPLICANT: Toroshimi
APPLICANT: Amann, Egone-Related Sulfatase-Like Protein and TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and TITLE OF INVENTION: Drocess for its Production
CORRESONDERS: 11
CORRESCENCE: Innegan, Henderson, Farabow, Garrett & STRE: D.C.
COUNTRY: USA
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STRE: D.C.
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: ERABABLE FORM:
COUNTRY: ERABABLE FORM:
COUNTRY: ERABABLE FORM:
COUNTRY: 18 PRICATION DATA:
APPLICATION NUMBER: US/08/411,887
FILING DATE: 28-AUG-1992
APPLICATION NUMBER: US -28-AUG-1992
APPLICATION UNMBER: US -28-AUG-1992
APPLICATION UNMBER: US -28-AUG-1992
APPLICATION UNMBER: US -28-AUG-1992
APPLICATION UNMBER: US -28-AUG-1992
APPLICATION U
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Score 42; DB 1; Length 533;
Pred. No. 72;
0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SUFFARE: Patentin Release #1.0, Version #1.25
SUFRENT ON THE PATENT NO. 1995
CLASSIFICATION NUMBER: 091.973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DidG10, Frank S
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DidG10, Frank S
FEEFERENCE/DOCKET NUMBER: 84162
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4366
TELEPHONE: 516-742-4366
TELEPHONE: 516-742-4366
TELER: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 maino acids
                                                                                                  APPLICANT: Morris, Charles P
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: HOPWOOG, JOhn J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF SEQUENCES: 15
CORRESSENDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                          E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08345212; Patent No. 5932211
GENERAL INFORMATION:
                                      Sequence 13, Application US/08484494; Patent No. 5798239; GENERAL INFORMATION:
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Bielicki, Julie
Clements, Peter R
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Morris, Charles
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Best Local Similarity 85.7
Matches 6; Conservative
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STRANDEDNESS: single
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US-08-345-212-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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63.6%; Score 42; DB 1; Length 533;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                           Score 42; DB 1; Length 533;
Pred. No. 72;
0; Mismatches 1; Indels
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MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Rclease #1.0, Version #1.25
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO: Frank S
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/COCKET NUMBER: 84162
TELECOMMUTCATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MOSTIS, Charles P
APPLICANT: MOSTIS, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: IDURONATE 2-SULFATASE
TITLE OF INVENTION: 15
CORRESSEDNIESCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York CUTY: USA
                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08484493
Patent No. 5728381
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                               63.6%;
85.7%;
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TYPE: amino acid
                                                               Query Match 63.6
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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US-08-445-586-10
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US-08-484-493-13
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Pred. No. 72;
0; Mismatches 1; Indels
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APPLICANT: O'BRIEN, JOHN S.

APPLICANT: TISHINGTO, YASUO
TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USAC

ZIF: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PLOPPY disk

COMPUTER: PLEM PC COMPATIBLE

COMPUTER: PER PC - DOS/MS-DOS

SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTING SYSTEM: US/08/100, 247

FILING DATE: 19930730

CLASSIFICATION NUMBER: US/08/100, 247

FILING DATE: 19930730

CLASSIFICATION: SAMATION:

NAME: ISTABLEN NUMBER: OBRIEN.002A

REGISTRATION NUMBER: OBRIEN.002A

REGISTRATION NUMBER: OBRIEN.002A

TELEPHONE: 619-235-0176

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

FUNCTH: 523 amino acids
                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,003
                                                                                                                                                                             CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,973
FILING DATE: 17-DEC-1992
ATTORNEY_AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOOKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPAN: 516-742-4343
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-100-247-2
; Sequence 2, Application US/08100247
; Patent No. 5571787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-249-003-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 YPGCGYW 450
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                                                                                                                                                                 FILING DATE:
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Pred. No. 72;
0; Mismatches 1; Indels
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City Plaza STATE: New York
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09249003
Patent No. 6153188
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Clements, Peter R
APPLICANT: Clements, Officer S
TITLE OF INVENTION: GLYCOSTLATION VARIANTS OF
TITLE OF INVENTION: IDDRONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:

CLASSIFICATION: 435
PILOR APPLICATION 1435
APPLICATION NUBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                       ZIP: 11530
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   دره، معدده
Best Local Similarity 85.7%;
Matches 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-345-212-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 YPGCGYW 450
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ZIP: 11530
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amino acid

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Sequence 2, Application US/08484594A
Fatent No. 5714459
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
APPLICANT: Kishimoto, Yasuo
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                      Sequence 3, Application US/08232513A
Patent No. 5700909
GENERAL INFORMATION:
PAPLICANT: O'BLIED JOHN S.
TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
TITLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4770 La Jolla Village Drive, Suite 700
CITY: San Diego:
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 523;
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC compatible
COMPUTER: IRW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
US-08-232-513A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERNCE/CDCKET NUMBER: P-UD 1643
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 62.5°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 CIWGPSYW 501
                                        494 CIWGPSYW 501
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1 cywgcgyw 8
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US-08-484-594A-2
                                                                                                        RESULT 8
US-08-232-513A-3
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Patent No. 5696080
GENERAL INFORMATION:
APPLICANT: O' SELIEN;
APPLICANT: O' SELIEN;
APPLICANT: O' SELIEN;
APPLICANT: CONTROLORY
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Blvd. 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                         Length 523;
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                       Score 40; DB 1; Length 523
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TEASTER: DOS
SOFTWARE: FASTER: DOS
SOFTWARE: OS/08/483,146A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYELOS.002DV1
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ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MY TELECOMMUNICATION: TELECOMMUNICATION: TELEPAN: 619-235-0176
                                                                                                                                                                                                                                       60.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: PROSAPOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.6
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                       Query Match 60.6
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                  TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         494 CIWGPSYW 501
                                                                                                                                                                                                                                                                                                                              1 cywgcgyw 8
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Length 30, 3; Indels

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APPLICANT: Anderson, W. French
APPLICANT: Baltrucki, Leon F.
APPLICANT: Baltrucki, Leon F.
APPLICANT: Mason, James M.
TITLE OF INVENTION: Targetable Vector Particles
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 62.5%; Pred. No. 17; 5; Conservative 0; Mismatches 3
      NAME: Sibley, Kenneth D.
REGISCRATION NUMBER: 31.665
REFERENCE/DOCKET NUMBER: 5470-134
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-50-2200
TELEFAX: 919-801-3175
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-753-829A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,126
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: 08/326,347
FILING DATE: 20-COT-1994
APPLICATION NUMBER: 08/326,347
FILING DATE: 09-NOV-1993
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Ecotropic gp70 Protein
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Patent No. 5985655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lillie, Raymond J.
REGISTRATION NUMBER: 31,778
REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 469 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201-994-1744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUCLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 becardITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CVWDGGYW 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-484-126-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Patent No. 5869250

GENERAL INFORMATION:
APPLICANT: Unliano, Rudolph L.
APPLICANT: Cheng, Xiaojun

TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF
TITLE OF INVENTION: PEPTIDES THAT RECOGNIZE SPECIFIC DNA SEQUENCES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Sellzer, Park & Gibson
STRRET: 1211 East Morehead Street
CITY: Charlotte
STATE: No. 5869250th Carolina
COUNTRY: United States

ZIP: 28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,829A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Lel
Pred. No. 1.3e+02;
0; Mismatches 3;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 5.23 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.6%;
62.5%;
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Best Local Similarity 62.50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-484-594A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        494 CIWGPSYW 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-753-829A-9
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Sequence 13, Application US/08895474

Sequence 13, Application US/08895474

Sequence 13, Application US/08895474

Setent No. 6136957

GENERAL INFORMATION:

APPLICANT: Nicola Nicola N.

APPLICANT: Gearing, David P.

APPLICANT: Gearing, David P.

APPLICANT: Ming, Julie Ann

TITLE OF INVENTION: Improvements in Granulocyte-Macrophage

TITLE OF INVENTION: Colony-Stimulating Factor Receptor and Derivatives Thereof

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                   UROGENITAL SINUS DERIVED GROWTH FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
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                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
                                                                                                   ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/008,348
FILLING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:
TELECHIONE: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35,723
3R: 34012.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICANT: ROWLEY, DAVID R. TITLE OF INVENTION: DROGENIT TITLE OF INVENTION: FACTOR N HUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.5
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                      COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino a STRANDEDNESS:
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27 CFDGCGY 33
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US-08-895-474-13
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Rastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMALIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                             Score 38.5; DB 2; Length 469;
Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 440;
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Pred. No. 2.9e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARDS DILLAR PROBLEM #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: CAING, EGA'IN P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET NUMBER: DX05520
TELEPHONE: 415.852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12. Application US/08761248B Patent No. 5958735
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08759628 Patent No. 6225446
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71.4%;
                                                                  58.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                               Query Match 58.3
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-759-628-4
                                                                                                                                                                                             174 YWGCETTGRAYW 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                   2 ywgc----gyw 8
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US-08-761-248B-12
    US-08-484-126-1
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US-08-759-628-4
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Sequence 57, Application US/08602999A

GENERAL INCOMMATION:

GENERAL INCOMMATION:

APPLICANT: SPAKE, Andrew B.

APPLICANT: THORN, Judith M.

APPLICANT: OUILLIAM, Lawrence A.

APPLICANT: DER, Channing J.

APPLICANT: POWLKES, Dana M.

APPLICANT: RIDER, James E.

TITLE OF INVENTION: SH3 BINING PEPTIDES AND METHODS OF

TITLE OF INVENTION: SH3 BINING SAME

NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennile & Edmonds

STREFF: NUMBERSEE: Pennile & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIERATION: 424
ATTORNEY AGENT INFERMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 1256.0030003
FELEMENCE-DOCKET NUMBER: 1256.0030003
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2500
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNES: peptide
US-08-895-474-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIREET: 1129 AVENUE OI THE AMERICAS
CIUTX: New York
STATE: New YORK
COUTRY: U.S.A.
2DP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1101-202
TELEFHONE: (212) 790-9090
TELEFRANC (212) 790-9090
TELEFRAN: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.8%; Score 35.5; D
Best Local Similarity 28.6%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:| | 111 | 4 CWWCCFFKWVQTRCKPDHGYW 24
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US-08-602-999A-57
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TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
TYPE
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Mon Aug 12 17:16:15 2002

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August 12, 2002, 17:13:22 ; Search time 24.99 Seconds (without alignments) 30.761 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                283138 seqs, 96089334 residues
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                10-071247-1
59
1 gywgkgyw 8
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                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                           Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries pir\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	in the state of th		T-cell receptor be	receptor	-cell receptor	-cell receptor	akinin - m	ţ	triacylglycerol li	tubulin beta-3 cha	T-cell receptor be	T-cell receptor be		T-cell receptor be	peptidylglycine mo	major fat-globule	pev-kinin 1 - pena	hypothetical pepti	•	leucokinin V - Mad	leucokinin VI - Ma	leucokinin VII - M	leucokinin VIII -	T-cell receptor be	r-cell receptor be	dissimilatory sulf	globulin IV alpha	Ig heavy chain CRD	T-cell receptor be
SUMMARIES	ID	TU0053	00000	DT0629	PT0728	A41946	B53284	A61068	PT0637	S57274	S33567	PT0628	PT0642	PT0722	PT0586	A38671	B48394	PD0029	155382	A31570	JS0315	JS0316	JS0317	JS0318	PT0724	PT0532	S63493	S09478	PT0278	PT0608
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	Score	25	2	200	20	19	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17			15	14	14	14
	Result No.	-	10	4 m	4	. r	9	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

2 ywgkg 6 ::[1] 3 FYGKG 7

ò QQ

H4 histone - Afric 640 Cerebellar degener 230 279 Igheavy chain (Trp-4, 279 Inceptor be 662 662 663 664 664 670 Inceptor be 671 Inceptor be 673 Inceptor be 7-cell receptor be 674 Inceptor be 675 Inceptor be 7-cell receptor be 677 Inceptor be 7-cell receptor be 678 Inceptor be 679 Inceptor be 7-cell receptor be 671 Inceptor be 671 Inceptor be 7-cell receptor be 671 Inceptor be 673 Inceptor be 674 Inceptor be 675 Inceptor be 677 Inceptor be 677 Inceptor be 678 Inceptor be 678 Inceptor be 679 Inceptor be 671 Inceptor be 672 Inceptor be 673 Inceptor be 674 Inceptor be 675 Inceptor be 677 Inceptor be 677 Inceptor be 678 Inceptor be 678 Inceptor be 678 Inceptor be 679 Inceptor be 671 Inceptor be 672 Inceptor be 673 Inceptor be 673 Inceptor be 674 Inceptor be 675 Inceptor be 677 Inceptor be 677 Inceptor be 678 Inceptor be 679 Inceptor be 670 Inceptor be 670 Inceptor be 670 Inceptor be 671 Inceptor be 671 Inceptor be 672 Inceptor be 673 Inceptor be 673 Inceptor be 674 Inceptor be 675 Inceptor be 677 Inceptor be 677 Inceptor be 678 Inceptor be 678 Inceptor be 679 Inceptor be 670 Inceptor be 671 Inceptor be 671 Inceptor be 672 Inceptor be 673 Inceptor be 673 Inceptor be 674 Inceptor be 675 Inceptor be 677 Inceptor be 677 Inceptor be 678 Inceptor be 679 Inceptor be 679 Inceptor be 670 Inceptor be 670 Incepto	Ando, M. isolated from	re 25; DB 2; Length 5; d. No. 2.8e+05; Mismatches 1; Indels 0; Gaps	mouse) se_revision 09-Mar-1990 #text_change 16-Aug-1996 se_revision 09-Mar-1990 #text_change 16-Aug-1990 #text_change 16-Au	re 22; DB 2; Length 7; cd. No. 2.8e+05; Mismatches 0; Indels 0; Gaps
151434 B356436 S21230 S21230 S21230 PT0211 PT03139 A61329 PT0618 PT0618 PT0671 PT1618 A41117 PH1618	1.; Mur 30, 828- 30, 828- 3206211 3 basal the gast	Score Pred. 1; Mis	couse e mouse) -revision 09-Ma Gilbert, M.; Te 86, 4624.4628, oolyreactive aut IUID:89282823	Score Pred. 2; Mis
(Ge) 222222222222222222222222222222222222	ta, 18, on c UID: UID:	44.0 .; ;	ouse e mc Gilk 86, UID:	38;
66 66 66 67 77 77 77 77 77 77 77 77 77 7	Commun Commun 1 function 10253; M Sin 10263; M Sin	42.4% larity 60.0% Conservative	(E7) - m as (hous as (hous 19, T.; u. U.S.A. atural p 33932; M	37.3%; Larity 60.0%; Conservative
22222222222222222222222222222222222222	and and other cote	arit	on Cult	ari1
	JH0253 Tkeda, T.; Dhys. Res. Cottorners and JH0253 JH0253 Ppe: proteir Ppe: proteir Fpe: proteir Fpe: proteir fill source: glis peptide circular means and periode for the proteir fill peptide circular means and periode for the periode for	1j.	cegic musc 11993 (3393) (4d. (4d. (4d. (4d. (4d. (4d. (4d. (4d.	Similarity 3; Conser
144 144 113 113 113 113 113 113 113 113	ika, T.; I ika, T.; I im. Blophy le. Struct trence num ssion: JH scule type idues: 1-5 brimental nent: This	atch cal gyw GFW	ESULT 2  g mu chain D region (E7) - mouse ;Species: Was musculus (house mouse); bate: 09-Mar-1990 #sequence_revision ;Accession: E3393 ;Hocorala, R.; Vo Quang, T.; Gilbert, Proc. Natl. Acad. Sci. U.S.A. 86, 4624 Title: Two murine natural polyreactiv; Reference number: A33932; MUID:89282E; Status: preliminary Molecule type: mRNA ;Residuos: 1-7 <bac> ;Cross-references: GB:M27106 ;Keywords: immunoglobulin</bac>	atch Sal
30 31 32 32 33 34 35 36 36 37 40 41 44 43 43 44 44 44 45 67 70 70 70 70 70 70 70 70 70 70 70 70 70	C) Acces R) Guesak Biochem A, Title A) Acces A) Acces A) Molec A) Exper C) Comme	Query M Best Lo Matches Qy 1 Db 1	RESULT 2 B33932 Ig mu chain D region (E7) - mouse C; Species: Mus musculus (house mouse C; Date: 09-War-1990 #sequence_revisi C; Accession: E3393 R; Baccala, R.; Vo Quang, T.; Gilbert Proc. Natl. Acad. Sci. U.S.A. 86, 46 A; Title: Two murine natural polyreac A; Reference number: A33932; MuID:892 A; Accession: E33932 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-7 - CAAC> A; Cross-references: GB: M27106 C; Keywords: immunoglobulin	Query Ma Best Loc Matches

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A;Molecule type: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Tr.dul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Speciesion: PT0728
R.Feeney, A.J.
T.Exp. Med. 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601
A.Reference number: PT0728
A.Reference number: RT0728
A.Reference number: RT0738
A.Reference num
                                                                                                                                                                                                                                                                       Ry Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601

A; Accession: PT0629

A; Accession: PT0629

A; Molecule type: mRNA

A; Residues: 1-6 <FEE>

A; Residues: 1-6 <FEE>

A; Accession: PT0528

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-6 <FEE>

A; Experimental source: adult thymus, strain BALB/c, clone 100-4AB

C; Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: A41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946
A;Accession: A41946
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                                                                                                                                                       C.Species: Mus musculus (house mouse)
C.Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Accession: PT0629; PT0528
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Pred. No. 2.8e+05;
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Pred. No. 2.8e+05;
); Mismatches 1; Indels
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Cyaccession: B51284
R.Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Title: Evolutionarily conserved organization and sequence conserved organization and sequence extracted from NCBI backbone (NCBIN:60738), NCBIP:60738)
C;Keywords: T-cell receptor
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A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, A;Reference number: A61068; MUID:92262851
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                                                                                                                 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May_1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
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C; Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F; 6/Modified site: amidated carboxyl end (Gly) #status experimental
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      Length
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llarity 100.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 0;
Score 19; DB 2;
Pred. No. 2.8e+05;
1; Mismatches 2
      Query Match 32.2%;
Best Local Similarity 50.0%;
Matches 3; Conservative
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Best Local Similarity
'....eq 2; Conserv?
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T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Dete: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Fence Med. 174, 115-124, 1991
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N region: A;Reference number: PT0509; MUID:91277601
A;Accession: PT0628
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Residues: 1-7 <FEE>
A;Residues: 1-7 <FEE>
A;Resperimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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C.Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Accession: Pr0642
R.Feener, A.J.
B.Exp. Med. 174, 115-124, 1991
A.Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions A.Reference number: Pr0642
A.Status: translation not shown
A.Mocession: Pr0642
A.Status: translation not shown
A.Mocession: Pr0642
A.Status: translation not shown
A.Mocession: Tr0642
A.Status: Tr0642
A.Status: Tr0642
A.Status: Tr0642
A.Status: Tr0643
A.Status: Tr0644
A.Status: T
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0722
R;Feeney, A.J.
J. Exp. Med. 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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                                                                                                                              3 GAKFW
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Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: Drosophila melanogaster
Cispecies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
Ciscossion: 833567
Rithuz, U.; Wolk, A.; Renkawitz-Pohl, R.
Development 116, 543-554, 1992
A;Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila vis A;Reference number: S33567; MUID:93170162
A;Reference number: S33567
A;Reference number: Sa3567
A;Reference number: S33567
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triacy1glycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C.Species: Psychrobacter immobilis
C.Species: Psychrobacter immobilis
C.Species: Psychrobacter immobilis
C.Accession: S57274
R.Arpigny, J.L.; Feller, G.; Gerday, C.
R.Arpigny, J.L.; Feller, G.; Gerday, C.
R.Arpigny, J.L.; Feller, G.; Gerday, C.
R.Aritle: Corrigandum to "Cloning, sequence and structural features of a lipase from the A.Reference number: S57274; MUID:95359197
A.Reference number: S57274
A.Reference preliminary
A.Reference preliminary
A.Residues: 1-7 <ARP>
A.Gross-references: EMBL:X67712
C.Keywords: carboxylic ester hydrolase
C: Accession: PT0637
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A: Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A: Reference number: PT0509; MUID:91277601
A: Accession: PT0637
A: Accession: PT0637
A: Molecule type: mRNA
A: Residues: 1-6 <FEE>
A: Experimental source: newborn thymus, strain BALB/C
C: Keywords: T-cell receptor
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C;Genetics:
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Pred. No. 2.8e+05;
1; Mismatches 2;
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A;Cross-references: FlyBase:FBgn0003888
A;Introns: 5/3
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Best Local Similarity 40.0%;
Matches 2; Conservative 1
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Best Local Similarity 100.v.
Thes 2; Conservative
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Matches 2; Conservative
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A38671

A38671

A38671

Deptidylglycine monooxygenase (EC 1.14.17.3) form 3 - rat (fragment)

C) Species: Rattus norvegicus (Norway rat)

C) Species: Rattus norvegicus (Norway rat)

C) Species: Rattus norvegicus (Norway rat)

C) Accession: A38671

C) Accession: A38671

A.Title: Characterization of novel mRNAs encoding enzymes involved in peptide alpha-amid A; Reference number: A38671; MUID:91107670

A.Accession: A38671

A.Status: preliminary; not compared with conceptual translation

A; Accession: A38671

A; Status: preliminary; not compared with conceptual translation

A; Residues: 17 < CMD

C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Species: Mus musculus (house mouse)
C. Species: No. 11-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Accession: PT0586; PT0592
B. Feeney, A.J.
C. Exp. Mad. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0586
A; Accession: PT0586
A; Accession: PT0586
A; Muscule type: mRNA
A; Molecule type: mRNA
A; Mesidues: 1-7 < FEE>
A; Residues: 1-7 < FEE>
A; Residues: 1-7 < FEE>
A; Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C; Keywords: T-cell receptor
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                                                                                                                                    Query Match 28.8%; Score 17; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
A; Residues: 1-7 <FEE>
A; Experimental source: newborn thymus, strain BALB/c
C; Keywords: T-cell receptor
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octopus min
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carcinus ma
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18691.

101-NOV-1990 (Rel. 16, Last sequence update)

101-NOV-1990 (Rel. 16, Last sequence update)

101-NOV-1990 (Rel. 16, Last sequence update)

101-NOV-1990 (Rel. 16, Last annotation update)

Angiotensin-converting enzyme inhibitor.

Thunnus albacares (Fallowfin tuna) (Neothunnus macropterus).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Acanthomorpha Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

NCBI_TAXID-8236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Corpora cardiaca;
MEDLINE-9226351; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
"Locustakinin, a novel myotropic peptide from Locusta migratoria,
isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
-!- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULAT
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                                                                                                                                                                                                                                                                                                                                               Locusta migratoria (Migratory locust).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acridoidea; Locusta.
P38644
P81864
P82657
P82655
P81860
P41841
P35904
P82158
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P42158
P42158
P42158
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6 AA; 654 MW; 686365A5B9CDB000 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                     6 AA.
                                                                                                                                                                                                   ALIGNMENTS
                         RE32_LITRU
ASP2_LACSN
AL17_CARMA
ALL5_CALVO
ACH1_ACHFU
OCP1_OCTMI
ALL7_CYDPO
                                                                                                                                        AL16_CARMA
ALL9_CARMA
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Conservative 0;
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MOD_RES 6 6
SEQUENCE 6 AA; 654 MW;
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TUBULES.
TOBOLES.
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Best Local Similarity
Matches 2; Conserv
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P41491;
01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-JUL-1998 (Rel.
Locustakinin I.
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ID ACI_THUAL
AC P1862
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DT 01-NO'
DT 01-NO'
DC CEUKAT'
OC EUKAT'
OC ACIIN
OC ACIIN
OC SCOMD
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P18691 thunnus alb
P21140 leucophaea
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Holman G.M., Cook B.J., Nachman R.J.; "Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of
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Best Local Similarity
Matches 2; Conserv
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Matches 2; Conserv
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"Isolation, primary structure and synthesis of two neuropeptides
from Leucophaea maderae: members of a new family of
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Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                  Leucokinin I (L-I).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea,
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8 AA; 893 MW; DC6365B449CDC76A CRC64;
                                                            Biochem. Biophys. Res. Commun. 155:332-337(1988).
PIR: A31570; A31570.
SEQUENCE 8 AA: 953 WW; 6AA863733051F1B7 CRC64;
                                                       Res. Commun. 155:332-337(1988).
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100.0%; Pred. No. 1e+05;
tive 0; Mismatches (
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100.0%; Pred. No. 1e+05;
iive 0; Mismatches (
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
10-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin II (L-II).
Leucokhaea maderae (Madeira cockraach).
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
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          TISSUE=Muscle;
MEDLINE-88326322; PubMed=3415688;
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P21141;
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P21140;
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LCK2_LEUMA
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-i- FUNCTION: THIS CEPHALDOWOTROPIC EPPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-i- SIMILARITY: TO THE OTHER LEUCOKININS.
Holman G.M., Cook B.J., Nachman R.J.; Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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01-WAY-1991 (Rel. 18, Last sequence update)
01-WAY-1991 (Rel. 18, Last annotation update)
Leucokinin III (L-III).
Leucophaea maderae (Madelra cockroach).
Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattarla; Blaberoidea; Blaberidae; Leucophaea.
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin IV (L-IV).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
NCBI_TaxID=6988;
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8 AA; 910 MW; DC6365B449C866DA CRC64;
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8 AA; 852 MW; DC6365A5B9C8676A CRC64;
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MOD_RES 8 8
SEQUENCE 8 AA; 852 MW;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattarla;
Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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P19989:
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LCK8_LEUMA
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01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Leucokinin V (L-V).
Leucokinin V (L-V).
Leucokinin whetazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blaberoidea; Blaberoidea; Leucophaea.
NCBI_TaxID=6988;
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8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;
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8 AA; 784 MW; 736365A5B9C865B8 CRC64;
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Pred. No. 1e+05;
0; Mismatches 0;
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Pred. No. 1e+05;
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Leucophaea maderae (Madeira cockroach)
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MOD_RES 8 8
SEQUENCE 8 AA; 906 MW;
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       SEQUENCE, AND SYNTHESIS,
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              TISSUE-Head;
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P19987;
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P19988;
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TISSUE-Head;

MEDLINE-87052651; PubMed-2877794;

MEDLINE-87052651; PubMed-2877794;

Hollman G.M., Cook B.J., Nachman R.J.;

Hollman G.M., Cook B.J., Nachman R.J.;

Isolation, primary structure, and synthesis of leucokinins V and VI:

myotropic peptides of Leucophaea maderae.";

Comp. Blochem. Physiol. B8C:27-30(1987).

- I- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND HELLOTHIS ZEA ADIPOKINETIC HORMONE.

- I- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND HELLOTHIS ZEA ADIPOKINETIC HORMONE.

M Neuropeptide; Amidation.

M Neuropeptide; Amidation.

M NOD_RES B AMIDATION.

SEQUENCE 8 AA; 935 MW; 9D636581E9D55A66 CRC64;
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Holman G.M., Cook B.J., Nachman R.J.;
Isolation, primary structure and synthesis of leucokinins VII and
VIII: the final members of this new family of cephalomyotropic
Peptides isolated from head extracts of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:31-34(1987).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARIY: JO THE OTHER LEUCOKININS.
PIR, JS0317; JS0317.
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VII (L-VII).
Leucokinin VII (L-VII).
Leucokinin VII (Rel. 17)
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID. AMIDATION. 9D6365B1E9D5A5A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
DC6365A5B9CDC76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
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Cýdia pomonella (Codling moth).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Futrygota; Neoptera: Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                 TISSUB=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
--- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
                                                                                                                                                                                                                       Mus musculus (Mouse).
Welaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.;
                                                                                                                                                01-OcT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-EPB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15; DB 1; Length 8;
Pred. No. 1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 1; Length 5;
Pred. No. 1e+05;
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922879CABB58640D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AA; 717 MW; 7364087043100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA.
                                                                                                             5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
NON TER 5 5
SEQUENCE 5 Aa; 717 MW; 73640R70A310
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Larva;
MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.4%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA; 898 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                               STANDARD;
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cydiastatin 5
                                                                                                           UF01_MOUSE
P38639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALL5_CYDPO
P82156;
 | | |
1 GSW 3
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RGY
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                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
ALL5_CYDPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                             UF01_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                        Holman G.M., Cook B.J., Nachman R.J.;

"Isolation, primary structure and synthesis of leucokinins VII and "Isolation, primary structure and synthesis of leucokinins VII and vIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";

Comp. Blochem. Physiol. 88C:31-34(1987).

-I- FUNCTION: FHIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-I- SIMILARITY: TO THE OTHER EDUCOKININS.

PIR, JS0318; JS0318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              octopus minor (Octopus).

Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda; Incirrata; Octopodidae; Octopus.
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                                                                                                         Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 1; Length 4;
Pred. No. 1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.8%; Score 17; DB 1; Length 8; 100.0%; Pred. No. 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 D-SERINE (IN OCP-4).
463 MW; 6AB365B81000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 8 AMIDATION.
8 AA; 902 MW; 736365AB59CAADD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 active than Ocp-3.

- SUBCELLULAR LOCATION: Secreted.
- PTM: Cop-4 has D-Ser instead of L-Ser.
- MASS SPECTROMETRY: WW-395.2; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
0ctopus minor (Octopus).
                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
   8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.4
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                               Leucokinin VIII (L-VIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10876044;
                                                                                                                                                                          Blaberoidea; Bla
NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain
                                                                                                                                                                                                                                                  TISSUE-Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
OCP3_OCTMI
ID OCP3_OCTMI
AC P58649;
LCK8_LEUMA
P19990;
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SEQUENCE,
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SEQUENCE
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fan Z. W., Eng J., Shaw G., Yalow R.S.;

"Cholecystckinin octapeptide purified from brains of Australian marsuplais.";

"Cholecystckinin octapeptide purified from brains of Australian marsuplais.";

"Peptides 9:429-431(1988).

-1- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION THE BEALN IS NOT CLEAR.

-1- FUNCTION: THE BRAIN IS NOT CLEAR.

-1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

RIN 743001; A43001.

RPROSTIE: PO0012; P00012.

RIN PROSTIE: PS00259; GASTRIN; 1.

RAMIDATION: MAIGHTION: HORMONE.

MOD_RES 8 AMIDATION.
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Submitted (APR-1999) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND 2: GH, GB, GC, GG, GD, GI, AND GE.
-!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                        CCK...

CCK...

Macropus eugenii (Tammar wallaby), and

Dasyuus viverinus (Southeastern quoll).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.

NCHL_TaxID=9315, 9279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
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P81780;
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 38, Last sequence update)
17-JUL-1999 (Rel. 38, Last sequence update)
18-JUL-1999 (Rel. 38, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
DDCAA68378768B5A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12; DB 1;
Pred. No. 1e+05;
0; Mismatches
                                                                                                                      10.1-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Cholecystokinin (CCK).
                                                                                                 8 AA.
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=88234141; PubMed=3375140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.3%;
llarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA; 1064 MW;
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA;
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                                                                                             CCKN_MACEU
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SEQUENCE.
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SEQUENCE
RESULT 14
CCKN_MACEU
ID CCKN_MACEU
DT 01-APR
DT 01-APR
DT 01-CPR
D
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DB 1; Length 8;

20.3%; Score 12;

Query Match

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Gaps
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                  1; Indels
ilarity 66.7%; Pred. No. 1e+05;
Conservative 0; Mismatches
 Best Local Similarity
Matches 2; Conserva
                                          4 gkg 6
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August 12, 2002, 17:14:38; Search time 39.45 Seconds (without alignments) 35.081 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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SPTREMBL\_19:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_invar:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_mhc:\* sp\_vertebrate:\*
sp\_unclassified:\* sp\_bacteriap:\* sp\_organelle:\* sp\_phage:\* sp\_plant:\*
sp\_rodent:\*
sp\_virus:\* sp\_archeap:\* sp\_rvirus:\* 

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

049223 glycine max P82685 periplaneta P82686 periplaneta P82686 periplaneta P82689 periplaneta P82689 periplaneta P82699 box faurus 095679 homo sapien 064971 alfalfa mos 045772 shigella dy 015888 homo sapien 002831 oryctolagus 095213 oryctolagus 095213 oryctolagus 095213 oryctolagus 090074 homo sapien 062721 rattus norv Description 049223 P82685 P82686 P82687 P82688 P82689 P82929 Q96RN9 Q96RN9 Q945R2 002831 095213 095945 09UCN4 Q62721 В Query Match Length 288.8 2288.8 2288.8 222.0 220.0 220.0 220.0 220.0 220.0 220.0 220.0 220.0 200. Score Result No. 

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TISSUE-CORPORA CARDIACA, MEDINE-98010462; PubMed-9350979; Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.; Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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MEDLINE-98010462; PubMed-9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopetroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
Neuropeptide; Amidation.
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-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-4 (PEA-K-4).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-3 (PEA-K-3).
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8 AA; 839 MW; 736365A5B9D6DDB CRC64;
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8 AA; 909 MW; DC6365B449D5A76A CRC64;
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MOD_RES 8 8
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MEDILINE-98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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Periplaneta americana (American cockroach).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Perryota; Neoptera; Orthopteroidea; Dictyoptera; Orthopteroidea; Blattoidea; Blattoidea; Blattoidea; Periplaneta.
                                                                                                                                        KININ-1 (PEA-K-1).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY SELONGS TO THE KININ FAMILY.
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
Neuropeptide; Amidation.
MOD_RES AM: 950 WW: 326365B449D58774 CRC64;
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--- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
--- SIMILARITY: BELONGS TO THE KININ FAMILY.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;
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TISSUE-CORPORA CARDIACA;
MEDLINE-98010462; PubMed-9350979;
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MOD_RES 8 8
SEQUENCE 8 AA; 856 MW;
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MEDLINE=21249095; PubMed=11350188; Corrigall A.V., Hitt. R.J., Davids L.M., Hancock V., Meissner D., Kirsch R.E., Meissner P.N.; "Identification of the First Variegate Porphyria Mutation in an Indigenous Black South African and Further Evidence for Heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus RNAs and the intercistronic junction in RNA 3.";
Nucleic Acids Res. 8:5635-5647(1980).
BELL: V00047; CAA23416.1; -.
NON TER
SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;
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MEDLINE-81124289; Pubmed-6927843;
Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,
Bol J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alfalfa mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Alfamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRUNCATED PROTOPORPHYRINOGEN OXIDASE (FRAGMENT).
                  935 MW; 9639D1A72058637D CRC64;
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ilarity 100.0%; Pred. No. 5.6e+05;
Conservative 0; Mismatches 0;
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Mol. Genet. Metab. 73:91-96(2001).
EMBL; AF321822; AAK69608.1; -.
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larity 66.7%;
Conservative
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"Small subunit of the mammalian mitochondrial riboscome. Identification
of the full complement riboscomal proteins present.";
Submitted (DEC-2000) to the SWISS-PROT data bank.
-! SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                       Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
Bos taurus (Bovine).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98010462; PubMed-9350979; Predel R., Gaede G.; Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.; "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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                                                                                       0;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-5 (PEA-K-5).
Friblaneta americana (American cockroach).
Periplaneta americana (American cockroach).
Petryoca; Neoptera; Orthopteroidea; Insecta;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       americana.";
Regul. Pept. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                          28.8%; Score 17; DB 5; Length 8; 100.0%; Pred. No. 5.6e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%; Score 17; DB 5; Length 8; 100.0%; Pred. No. 5.6e+05;
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8 AA; 865 MW; C76365B449CDC775 CRC64;
                                                                                                                                                                                                                                                                                     8 AA.
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SIMILARITY: BELONGS TO THE KININ FAMILY
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                       Query Match
Best Local Similarity 100...
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MOD_RES 8 8
SEQUENCE 8 AA; 865 MW;
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Matches 2; Conservative
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TISSUE-CORPORA CARDIACA;
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TISSUE=LIVER;
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STRAIN=F-I/RGM;
Mage R.G., Chen H.-T., Alexander C.B., Chen F.F.;
"Rabbit DQS2 and DH Gene Rearrangements in Early B-cell Development.";
MO1. Immunol. 0:0-0(1996).
EMBL; U62585; AAB18735.1; -.
                                                                                                                                                                                                                                                                     Vuorio E.;
"Evidence for insufficient chondrocytic differentiation during repair
of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996).
EMBL; S83371; AAD14433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last annotation update)
PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96377339; PubMed-8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GERMLINE DH (DF) GENE (FRAGMENT)
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8 AA; 1028 MW; B859C7272EA77371 CRC64;
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50.0%;
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Best Local Similarity
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Best Local Similarity
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SEQUENCE FROM N.A.
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Polard P., Prere M.F., Chandler M., Fayet O.;
Programmed translational frameshifting and initiation at an AUU codon in gene expression of bacterial insertion sequence IS911.";
J. Mol. Biol. 222:465-477(1991).
SEQUENCE 8 AA; 902 MW; FE2DCAFB586AE336 CRC64;
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"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL: L12069; AAA73878.1; -.
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                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          OBRSE2;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

31,000 DA PRODUCT OF ORFB.

Shigella dysenteriae

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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            Length 8;
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          Score 15; DB 12;
Pred. No. 5.6e+05;
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            25.4%;
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8 AA; 1068
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TISSUE-PLACENTA;
                           Best Local Similarity
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NCBI_TaxID=622;
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Q15888;
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Q15888
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Mitochondrion.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE.

Raboudi N., Julian J., Rohde L.H., Carson D.D.;

Nidentification of cell-surface heparin/heparan sulfate-binding proteins of a human uterine epithelial cell line (RL95).";

SEQUENCE 8 AA; 689 MW; 8088733DD33DD87D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL-SURFACE HEPARIN/HEPARANSULFATE-BINDING PROTEIN PEPTIDE (FRAGMENT).
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                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INSIDE INTRON 5 (FRAMBLT).
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SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;
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50.0%;
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Best Local Similarity 50.0
Matches 3; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:\*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:\*
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12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
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17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
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19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Fluorine-18 (F-18)	Imminogenic pentid	F1001100-18 (F-18)	Tmminogenia pentid	RGD Conta pentide	Lvcium B nentide	Moraxella catarrha	Moraxella catarrha	Core no voentide f	Viral DP178/107-1;
SUMMARIES	ID	AAY03714	AAY03716	AAY76818	AAY03715	AAY76817	AAR57814	AAR11895	AAW46276	AAW46279	AAY89518	ABB00926
	DB	20	20	21	20	21	15	12	19	19	21	22
	Query Match Length DB	80	80	80	8	œ	9	00	7	80	ω	æ
æ	Query	100.0	100.0	86.4	76.3	76.3	55.9	50.8	47.5	47.5	47.5	47.5
	Score	59	59	51	45	45	33	30	28	28	28	28
	Result No.	-	7	m	4	2	9	7	80	σ	10	11

11-MAR-1999.

12 28 47.5 8 22 ABB02392 13 28 47.5 8 22 AAU13472 15 27 45.8 6 15 AAR57919 17 27 45.8 6 15 AAR57913 18 27 45.8 6 15 AAR57813 19 27 45.8 6 15 AAR57813 20 26 44.1 6 13 AAR20449 21 26 44.1 6 13 AAR20449 22 24 26 44.1 8 18 AAW22884 24 26 44.1 8 18 AAW22883 25 42.4 6 13 AAR2083 25 42.4 6 13 AAR2083 25 42.4 6 13 AAR3039 25 42.4 6 19 AAW30356 33 25 42.4 6 19 AAW30356 34 25 42.4 6 19 AAW30356 35 42.4 6 19 AAW30356 36 25 42.4 6 19 AAW30356 37 25 42.4 6 19 AAW30356 38 25 42.4 6 19 AAW30356 39 25 42.4 7 10 AAP91775 42 4 7 10 AAP91775 42 4 7 10 AAP91775 42 4 8 19 AAW50463 43 25 42.4 8 19 AAW30340 44 25 42.4 8 19 AAW50403 45 42.4 8 19 AAW50465 46 25 42.4 8 19 AAW50463 47 25 42.4 8 19 AAW50463 48 25 42.4 8 19 AAW50463 48 25 42.4 8 19 AAW50465 49 AAWS0340 40 AAW30340 41 25 42.4 8 19 AAWS0340	Viral core polypep DP178-like/DP107-1 Core polypeptide T RGD contg. peptide RGD contg. peptide RGD contg. peptide	RGD contg. peptide G. oxydans cytochr Anti-b-endorphin m Beta-endorphin N-t Membrane dipeptida	peptid peptid peptid de corr ogenic b-endor	Snake venom derive Snake venom derive Snake venom derive Snake venom derive Synthetic SCM-acti Synthetic SCM-acti A. diadematus fibr S11k spider fibroi	ynorphin-li nake venom -cell recep nake venom nake venom nake venom uman ART-l
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	22 ABB02 22 AAU13 22 AAB77 15 AAR57 15 AAR57	15 AAR57 22 AAY97 13 AAR20 16 AAR70 20 AAY48	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	19 AAX1596 19 AAW5041 19 AAW5041 10 AAW5035 10 AAP9177 10 AAY3339 22 AAU0903	15 AAK6104 19 AAW1595 19 AAW5762 19 AAW5046 19 AAW5040 19 AAW5034 21 AAB0389
	2 28 47. 28 47. 28 47. 5 27 45. 6 27 45.	8 27 45. 0 26 445. 2 26 444. 2 26 444.	25 26 44. 25.5 44. 25.5 44. 25.5 44.	25 42. 25 42. 3 25 42. 3 25 42. 25 25 42.	25 42. 25 25 42. 26 25 25 42. 27 25 25 42. 27 25 25 42.

## ALIGNMENTS

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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                         /note= "D-form residue; optionally has a free protected amino acid group"
                                                                                                                                                                     /note= "optionally has a free or protected amino acid group"
                                                                                                                                                                                                    /note= "D-form residue"
                                                                                                                                                                                                                        /note= "D-form residue"
                                                                                                                                                                                                                                                                                            /note= "D-form residue"
                                                                                                                                                                                                                                                                        /note= "D-form residue"
                                                                              Fluorine-18 (F-18) labeled peptide 1.
                                                                                                                                                    Location/Qualiflers
                    AAY03714 standard; peptide; 8 AA.
                                                           (first entry)
                                                                                                                                                                                       Misc-difference 2
                                                                                                                                                   Key
Misc-difference 1
                                                                                                                                                                                                                                                             Misc-difference 7
                                                                                                                                                                                                                                                                                 Misc-difference 8
                                                                                                                                                                                                             Misc-difference 3
                                                                                                                                                                                                                                 Misc-difference 5
                                                                                                                                                                                                                                                                                                               WO9911590-A1
                                                           08-JUN-1999
                                                                                                                               Synthetic
                                       AAY03714;
             AAY03714
RESULT
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(IMMU-) IMMUNOMEDICS INC.
                       /note=
                                                                                                                                                                                                                       WPI; 1999-228967/19.
                                 Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA;
          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 думдкдум 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-1998;
                                                                                                                                               03-SEP-1997;
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                                                                      W09911590-A1
                                                                                               11-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY76818;
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δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            throp peptide-containing tergeting vectors for use in clinical positron emission tenders. Use amerinou for incorporating the relationship tergeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with formprises reacting a peptide comprising a free thiol formula: 18F-(CH2)m-CRIR2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bears at least one leaving group comprising i. Br. Cl. azide, tosylate, mesylate, mesylate, nosylate, triflate, m = 0-2; n+m = 0-2; x = 1, Br. Cl, azide, tosylate, mesylate, nosylate, triflate, maleimide (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl. R2 = 1, Br. Cl, azide, tosylate, mesylate, triflate, triflate, maleimide CC (optionally substituted by CONH2, cONH2, conf. of, sulfonic acid, tertiary amine, quaternary ammonium, alkyl

CC (optionally substituted by CONH2, CONH2, of, sulfonic acid, tertiary amine or quaternary ammonium), COOR', CONH2, or Sulfomic acid, tertiary amine or quaternary ammonium), COOR', CONH2, or COR', and R' = 1-6C alkyl or phenyl. The method is used for Radiolabeling peptide-containing receptor-targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the nutural pH and moderate temperature, sequences AAY0374-716 represent examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                      radionuclide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 59; DB 20; Length 8 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                      Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                     The invention relates to a method for incorporating 18F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "D-form residue; D-iodo-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-terminal acetylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fluorine-18 (F-18) labeled peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY03716 standard; peptide; 8 AA.
                                                                                                                                                              Claim 13; Page 15; 22pp; English.
             98WO-US18268
                                    97US-0057485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                             (IMMU-) IMMUNOMEDICS INC
                                                                                                             WPI; 1999-228967/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 gywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gywgkgyw 8
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Modified-site
             03-SEP-1998;
                                    03-SEP-1997;
                                                                                      Griffiths GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY03716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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ID AAY0:
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The invention relates to a method for incorporating 18F radionuclide into peptide-containing targeting vectors for use in clinical positron comparably. Radiolabeling thiol-containing peptides with floating the comprising a free thiol fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CRIR2-(CH2)n-X, or carbon atoms bears at least one leaving group comprising I. Br. Cl. azide, tosylate, mosylate, nosylate, no method is Br. Cl. azide, tosylate, mosylate, nosylate, nosylate, melainide (coptionally substituted by 1-2 alkyl) or 3-ulfomaleimide; RI, RZ = I, CL, azide, tosylate, mosylate, riflate, H, CONH2, COOH, CO, sulfonic acid, tertiary amine, quaternary ammonlum, alkyl contionally substituted by CONH2, COOH, OW, sulfonic acid, tertiary amine, quaternary ammonlum, alkyl coptionally substituted by CONH2, or COR, and RY = 1-6C alkyl or phenyl. The method is used for Radiolabeling peptide-containing trageting vectors such as proteins, antibodies, antibody fragments and receptor targeted peptides for use in routine clinical positron comparapy. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAV03714-716 represent termorating a them thod of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic peptide; bl-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
/note= "D-form residue; optionally acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                "D-form residue; D-iodo-Tyr'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                        /note= "D-form residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY76818 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 15; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US18268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0057485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating a bi-specific diseased tissues in a patient comprising administering a bi-specifically antibody (or fragment) having at all least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bi-specific antibodies that bind specific target tissue and targeted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On 2;
                                                                                                                                                                           'note= "acetylated D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 21; L
Pred. No. 6.4e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McBride WJ,
                                                                                                "D-form iodo-Tyr"
                                                                                                                                                                                                                'note= "D-form iodo-Tyr"
                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                     /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fluorine-18 (F-18) labeled peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leung S,
                      Location/Qualifiers
                                                         /note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY03715 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              98US-0090142.
98US-0104156.
                                                                                                                                                                                                                                                                                                                                                                         99WO-US13879,
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ilarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffiths GL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMUNOMEDICS INC.
                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-160561/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                         Misc-difference 2
                                                                                                                                                                                            Misc-difference 7
                                                                                                                                                     Misc-difference
                                                                                                                  Misc-difference
                                                                                                                                                                                                                                Misc-difference
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                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                29-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hansen HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conjugates
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ID AAY0
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AC AAX0
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DT 08-J
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into peptide-containing targeting vectors for use in clinical positron cantsion tomography. Radiolabeling thiol-containing peptides with carission tomography. Radiolabeling thiol-containing peptides with carission tomography. Radiolabeling thiol-containing peptides with carission tomography. Radiolabeling thiol-containing peptides with a labeling reagent of formula: 18F-(CH2)m-CRIR2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bears at least one leaving group comprising I, Br, Cl, azide, tosylate, nosylate, or triflate, n = 0-2; n+m = 0-2; x = 1, Br, Cl, azide, tosylate, mosylate, orsylate, triflate, maleimide (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl, R2 = I, Br, Cl, azide, tosylate, mesylate, nosylate, triflate, H, CONH2, COOH, OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl or or quaternary ammonium, cOOK, COOH, OH, sulfonic acid, tertiary amine, corresponded for Radiolabeling peptide-containing correspond is used for Radiolabeling peptide-containing creeptor targeting vectors such as proteins, antibodies, antibody fragments and erceptor targeted peptides for use in routine clinical positron containing property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY03714-716 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó;
18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
                                                                                                                                                                                                                /note= "N-terminal acetylation; optionally has a free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for incorporating 18F radionuclide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "D-form residue; optionally has a free or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 20; Length 8;
Pred. No. 6.4e+05;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                                                       or protected thiol group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protected thiol
                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "D-form residue"
                                                                                                                                                                                                                                                                                                            /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "D-form residue"
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Page 15; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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illarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US18268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-228967/19.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 5
                                                                                                                                                         Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9911590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1998;
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Query Match
Best Local Similarity
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                                                                                                                      2 ywgcgyw 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1992;
18-AUG-1993;
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1 wgrgdw
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                                                                                                                                                                                                                                                                                                                      03-OCT-1994
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                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                            AAR57814;
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                                        Matches
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                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable complex, therapeutic agent or diagnostic antibodies against a targetable complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                              _note= "acetylated; modified with free amino acid group,
protected amino acid group, chelating agent or a
metal-chelate complex"
                                                                                                                                                                                                                               Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "D-form residue; modified with free amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                                         Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                          AAY76817 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 61; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0090142.
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                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMU-) IMMUNOMEDICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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14-OCT-1998;
                                                                                                                                               28-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-DEC-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugates
                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                    AAY76817;
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                                   AAY76817
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                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptides given in AAR57801-28 have antithrombotic, anticoagulant
                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides and their salts - used in platelet prepns., as antithrombotic agents and as inhibitors of e.g. cell adhesion, cancer metastasis and extracorporeal circulation coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Platelet; antithrombotic; inhibitor; cell adhesion; cancer; metastasis; extracorporeal circulation; coagulation; anticoagulant; cell fusion.
76.3%; Score 45; DB 21; Length b; 85.7%; Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 15; Length 6;
Pred. No. 6.4e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cell fusion inhibiting effects. They may be used in
antithrombotic agents and as extracorporaal circulation
coagulation inhibitors, cell adhesion inhibitors, cancer
metastasis inhibitors and protecting agent in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGD contg. peptide having antithrombotic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 52; 88pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR11895 standard; Protein; 8 AA.
                                                                                                                                                                                                                                                                                                 AAR57814 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YAWA ) NIPPON STEEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1991 (first entry)
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preparations. (IC50 = 2.2 \times 10 -5 M).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katada J, Sato Y;
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This peptide corresponds to amino acid residues 296-302, in the non-conserved region 1, of the outer membrane protein CopB (see AMW4621) of Moraxella catarrhalis strain 035E. Claimed isolated peptides of about 5-60 amino acid residues comprise at least this 7-amino acid peptide sequence and are reactive with monoclonal antibody 10F3. The 7-amino peptide is most preferred for binding to 10F3. It is located C-terminal to the Asn-295 cesidue of CopB that influences the binding kinetics of the epitope. Peptides which contain residues C-terminal to Asn-295 retain reactivity, but this reactivity is less than that obtained in the presence of Asn-295. Claimed peptides (see AAW46274-84) from non-conserved region 1 can be used in the diagnosis, prophylaxis (as vaccines) and treatment of M. catarrhalis infections.
                                                                                                                                          New isolated Moraxella catarrhalis peptide(s) - which define epitopes of the outer membrane protein used to develop products for the diagnosis, prophylaxis and treatment of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Moraxella catarrhalis peptide(s) - which define epitopes of the outer membrane protein used to develop products for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane protein; epitope; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 19; Length 7; Pred. No. 6.4e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis CopB region I epitope.
                                                                                                                                                                                                      Claim 3; Page 113; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moraxella catarrhalis strain 035E.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW46279 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.5%;
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             96US-0023832
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                                             (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                           WPI; 1998-159542/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-159542/14.
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                                                                             Cope LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA;
           12-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ywgkgy 7
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2 yagkgy 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2-AUG-1997;
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                                                                             Aebi C,
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                                   Lycium; angiotensin converting enzyme; renin; hypertension; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This lycium B peptide has angiotensin converting enzyme (ACE) and renin inhibiting activity and can be used in the treatment of hypertension. It is used in the form of a drug compsn. Residue 4 (GIY) is modified by calcium and residue 8 (Trp) has an indol gp.
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therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) lyciumin A and B - have ACE and renin inhibiting activity for treatment of hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 12; Length 8; Pred. No. 6.4e+05; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella catarrhalis CopB region I epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                 /note= "tryptophan indol"
                                                                                                                      'note= "pyroglutamyl"
                                                                      Location/Qualifiers
                                                                                                                                                                     /note= "glycyl Ca"
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; page 1; 6pp; Japanese.
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/label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-144847/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAR11894.
     Lycium B peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
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WO200164013-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001
                                                                                                                                                                                    3 wgkgy
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                                                                                                        Sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are dearlyed from various retroviral envelope (9p41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacoligically useful peptide for the treatment or prevention of a disease. The core polypeptides are bloactive peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                           Retrovirus; hybrid polypeptide; enhancer; 9p41; envelope protein; HIV-1; HIV-2; SIV; pharmacokinetic; half-11fe; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.
                                                                                                                                                                                                                                             Gaps
                                                     non-conserved region 1, of the outer membrane protein CopB (see AAW46271) of Moraxella catarrhalis strain 035E. Claimed isolated peptides of about 5-60 anino acid residues comprise at least this 8-amino acid residues comprise at least conscional antibody 10F3. The 8-amino peptide is most preferred for binding to 10F3. It includes the ABT-295 residue of CopB that is required for 10F3 binding. Claimed peptides (see AAW46274-84) from non-conserved region 1 can be used in the diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence -
                                              This peptide corresponds to amino acid residues 295-302, in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lambert DM;
                                                                                                                                                                                                                     Score 28; DB 19; Length 8;
Pred. No. 6.4e+05;
0; Mismatches 1; Indels
the diagnosis, prophylaxis and treatment of infection
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                                                                                                                                                                                                                                                                                                                                                                                                                      Core polypeptide fragment T No. 1076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 39; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merutka G,
                       Claim 6; Page 113; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                  AAY89518 standard; peptide; 8 AA.
                                                                                                                                                                                                                       47.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TRIM-) TRIMERIS INC.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                       8 AA;
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3 yagkgy 8
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                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2000
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                                                                                                                                                                infections
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                                                                                                                                                                                                                                                                                                                                                                         AAY89518;
                                                                                                                                                                                       Sequence
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selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or anglogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV; virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 21; Length 8;
Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-terminal is substituted by Ac"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral DP178/107-like region peptide T1076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB00926 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity
Matches 4; Conserv
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Sequence

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The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus I (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention corresponds to amino acids 588-595 of gp41 from HIV-1LAI. The invention of correction of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antilusogenic, antifusogenic, artivital or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The presents sequence represents one of the DP178-like/DP107-like peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a compound that inhibits the formation of or disrupts a DPIO/7/DPI78 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DPI07/DPI78 complex
                                                                                                                                                                                                                                  Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifusogenic; antiviral; HIV transmission; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 22; Length 8; Pred. No. 6.4e+05; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                Human immunodeficiency virus 1 isolate LAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                           DP178-like/DP107-like peptide T-1076.
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                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                    AAU13472 standard; Peptide; 8 AA.
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80.0%;
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                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated analogues of the heptad repeat region peptides pp178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-ILAI transmembrane protein gp41. The HR1 and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
infection.
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antczak JB, Delmedico MK, Erickson JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viral core polypeptide, SEQ ID NO: 919.
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                                                                                                                                                                                                                                                                                                                          ABB02392 standard; Peptide; 8 AA.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002 (first entry)
                                                                                              Query Match 47.5
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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the specification.
                                        8 AA;
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3 wgygy 7
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Gaps ; 0

Sequence

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(first entry)

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cancer; metastasis; extracorporeal circulation; coagulation; anticoagulant; cell fusion.
                                                                                                                                                               Platelet; antithrombotic; inhibitor; cell adhesion;
                                                                                                                      RGD contg. peptide having antithrombotic activity.
AAR57812 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YAWA ) NIPPON STEEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-101121/12
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                                                                                                                                                                                                                                                                                                                                                                      07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-1992;
18-AUG-1993;
                                                                               03-OCT-1994
                                                                                                                                                                                                                                                                                      WO9405696-A.
                                                                                                                                                                                                                                                                                                                               17-MAR-1994.
                                                                                                                                                                                                                                                  Synthetic.
                                         AAR57812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide when core polypeptides can be used for modulating fusogenic events and intracellular processes involving coiled-coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus, elegatics wirus, mason-pfizer virus and polio virus).

The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side effects.

In which that we are not assertivity of the diagnostic procedure is the character of the sensitivity of the diagnostic procedure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core
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                                                                                                                                                                                                                            Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatchropic; antiinflammatcry; hybrid polypeptide; coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merutka G, Anwer MK, Lambert DM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 51; 151pp; English.
                                                              AAB77919 standard; Peptide; 8 AA
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                                                                                                                                                   (first entry)
                                                                                                                                                                                       Core polypeptide T1076.
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                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                           AAB77919
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93WO-JP01262. 92JP-0238624.

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                                                                                                                                                   The peptides given in AAR57801-28 have antithrombotic, anticoagulant and cell fusion inhibiting effects. They may be used in antithrombotic agents and as extracorporeal circulation coagulation inhibitors, cell adhesion inhibitors, cancer metastasis inhibitors and protecting agent in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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New peptides and their salts - used in platelet prepns., as antithrombotic agents and as inhibitors of e.g. cell adhesion, cancer metastasis and extracorporeal circulation coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 12, 2002, 17:14:32 Job time: 245 sec
                                                                                                     Disclosure; Page 52; 88pp; Japanese
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Similarity 50.0%;
3; Conservative
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RESULT 15 AAR57812

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Sequence 22, Appl Sequence 21, App Sequence 919, Appl Sequence 919, Appl Sequence 9, Appli Sequence 9, Appli Sequence 28, Appl Sequence 28, Appl Sequence 39, Appl Sequence 19, Appl Sequence 225, Appl Sequence 225, Appl Sequence 225, Appl Sequence 11, Appl Sequence 6, Appl Sequence 11, Appl Sequence 
                                                                                                     August 12, 2002, 17:12:17; Search time 20.43 Seconds (Without alignments) 9.565 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-358-160-227
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US-08-014-426-28
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US-08-014-426-28
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US-08-462-661A-19
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US-08-525-539A-39
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US-08-358-160-225
US-08-359-160-211
US-08-350-260A-14
US-08-463-230A-4
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		icat	ton:	FRENKEL, GRANT, W	SAVIN, KE	LION	ADDRI FOLEY	re 5 NDRI	INIA ITED	)299 3LE	FI 3M P	STEM	VIIONB	. 2	NO	26	26 26	UMB	26 0N	TUMB 26	ON	26	TUMB 26	ON	26 INF
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44444444666666666666666666666666666666		046-22 22, Applic	1. 5948644 INFORMATION: ANT: DOPHETDE:	APPLICANT: APPLICANT:	ANT:	P. I.	CORRESPONDENCE ADDRE ADDRESSEE: FOLEY	ET:	E: , PRY:	223 ER RE	JM TY	ATING	CAT	VG DZ	APPL.	NG DP	ICATI	APPLI [CAT]	NG DA	CATI	CATI	IG DA	CATI	IOR APPLICATION DA	IG DA
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Anwer, M.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
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GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Ameutka, Gene
APPLICANT: Amer, Modmed
APPLICANT: Ambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
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TITLE OF INVENTION: HYBRID POLYPEPTIDES
CURRENT PELING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 919
LENGTH: 8
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Pred. No. 1.7e+05;
0; Mismatches 1;
                   REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: LEY=1
TELECOMMULICATION INFORMATION:
TELECHONE: 202-628-5197
TELEPA: 24863
TELER: 24863
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 maino acids
TYPE: anino acids
TYPE: TINEAT
MOLECULE TYPE: Protein
US-08-358-160-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 919, Application US/09315304B; Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 919, Application US/09082279B Patent No. 6258782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-919
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Best Local Similarity 80.0%;
Matches 4; Conservative (
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MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC COMPATIBLE
COMPUTER: THEN PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR REPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/240,160
FRANCE APPLICATION NUMBER: US 07/240,160
FRANCE APPLICATION NUMBER: US 07/240,160
FRANCE APPLICATION NUMBER: US 07/240,160
                                                                                                                                                                    LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichostrongylus colubriformis
US-08-467-046-22
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7*
Matches 4; Conservative
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US-08-358-160-227
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NESOUR 6

US-09-258-754-9

Sequence 9, Application US/09258754

Patent No. 6174687

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erki

APPLICANT: Rajotte, Daniel

TITLE OF INVENTION: Membrane Dipeptidase

TITLE OF INVENTION: Membrane Dipeptidase

TITLE OF INVENTION: NUMBER: US/09/258,754

CURRENT FILING DATE: 1999-02-26

EARLIER APPLICATION NUMBER: 09/042,107

EARLIER PILING DATE: 1999-03-13

NUMBER OF SEQ ID NOS: 452

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09042107

Beatent No. 623287

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Tissues

FILE REFERENCE: P-LJ 2892

FILE REFERENCE: P-LJ 2892

CURRENT APPLICATION UNDABER: US/09/042,107

CURRENT FILING DATE: 1988-03-13

NUMBER OF SEQ ID NOS: 436

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 7

LENGTH: 7

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-9
           Score 26; DB 1; Length 6; Pred. No. 1.7e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.1%; Score 26; DB 4; Length 7; 80.0%; Pred. No. 1.7e+05; Live 0; Mismatches 1; Indels
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           A4.18;
Similarity 75.08;
3; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                            Best Local Similarity Matches 3; Conserv
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Matches 4; Conserv
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2 GFWG 5
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                                                                                            1 gywg 4
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             Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/718,577
FILING DATE: 19910620
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One Market Plaza, Steuart Street
Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dower, William J.
APPLICANT: Dower, William J.
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
TITLE OF INVENTION: SCREENING SYSTEMS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROR APPLICATION 1919

APPLICATION NUMBER: US 07/541,108
FILING DATE: 20-UNU-1990
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFERRUCE/DOCKET NUMBER: 11509-25-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETHONE: (415) 326-242
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                        CURRENT APPLICATION NUMBER: US/09/315,304B
                                     CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 8
                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Core polypeptide US-09-315-3048-919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/07718577 Patent No. 5432018 GENERAL INFORMATION:
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                         47.5%;
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Best Local Similarity 80.0
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-718-577-2
FILE REFERENCE: 7872-052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105-1492
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3 WGYGY 7
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STATE:
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Sequence 9, Application US/08232261
Patent No. 5498601
GENERAL INFORMATION:
APPLICANT: Sato, Yoshim
APPLICANT: Katada, Jun
TITLE OF INVENTION: Aggregation-Inhibiting Agents, Blood
TITLE OF INVENTION: Coagulation-Inhibiting Agents, Blood
TITLE OF INVENTION: Circulation, Cell Adhesion-Inhibiting Agents, Tumor
TITLE OF INVENTION: Aggregation-Inhibiting Agents, Tumor
TITLE OF INVENTION: Aggregation-Inhibiting Agents, Tumor
UNDBER OF SQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                           COMPUTER REALBLE FORD

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: STERM: PC-DoS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01319

FILING DATE: 04-FEB-1994

APPLICATION NUMBER: US 08/014,426

FILING DATE: 05-FEB-1993

ATONEX/AGENT INFORMATION:

NAME: SAILH, Willaim M

REGISTRATION NUMBER: 30,223

REGISTRATION NUMBER: 30,223

RELEPHONE: (415) 326-2400

TELEPHONE: (415) 326-2400

TELEPACH POR SEQ ID NO: 28:

SEQUENCE CHARATENISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mr. Edward W. Greason, Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,261
FILING DATE: 06-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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STREET: One Broadway
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                             COMPUTER READABLE FORM:
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
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APPLICANT: Beatt, Renesch
APPLICANT: Bratt, Renesch
APPLICANT: Bratt, Renesch
APPLICANT: Bratt, Renesch
APPLICANT: Dower, William
TITLE OF INVENTION: RECEPTIDES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITX: Palo Alto
                                                                                                                                                                                                                                                     APPLICANT: Renschler, Markus F.
APPLICANT: Levy, Ronald
APPLICANT: Levy, Ronald
APPLICANT: Davy, Ramesh
APPLICANT: Daver, William
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REABLE FORM:

MEDIUM TRYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/014,426
FILING DATE: 05-FEB1993
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willeam M
REGISTRATION NUMBER: 5490A-204
TELEPANCE COCKET NUMBER: 5490A
TELEPANCE: (415) 326-242
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: ATTORNEY AINCHES
TYPE: ATTORNEY AI
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; Sequence 28, Application PC/TUS9401319
; GENERAL INFORMATION:
                                                                                                                                                           Sequence 28, Application US/08014426 Patent No. 5512435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.1%;
ilarity 42.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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Best Local Similarity
Matches 3; Conserv
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3 GKWGK
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Fatent No. 5747447
FEBERAL INFORMATION
APPLICANT: SWIFT, ROBERT L.
APPLICANT: BU MEE, CHARLES P.
APPLICANT: RANDOLPH, ANNE
TITLE OF INVENTION: STABLE POLYPEPTIDE COMPOSITION
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALLO SQUARE, 3000 El Camino Real
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                 Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.4%; Score 25; DB 6; Length 6; 80.0%; Pred. No. 1.7e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
5318899-55
;Patent No. 5318899
; APPLICANT: SCARBOROUGH, ROBERT M.;WOLF, DAVID L.;CHARO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ISRAEL F: JUNEAUT: SCARBORNOUGH, NOBERT M.; MOLE, DAVID L.; CHARC, TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS NUMBER OF SEQUENCES: 83 ; CURRENT APPLICATION NUMBER: US/07/483,229 | FILING DATE: 20-FEB-1990 | PRIOR APPLICATION NUMBER: 418,028 | FILING DATE: 06-OCT-1989 | FILING DATE: 16-JUN-1989 | FILING DAT
                                                                                                                           Score 25; DB 1; 1
Pred. No. 1.7e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/462,661A
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/055,636
FILLING DATE: 30-APRIL-1993
APPLICATION NUMBER: US 07/876,625
FILLING DATE: 30-APRIL-1992
                                                                                                                              42.4%;
80.0%;
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Best Local Similarity 80.07
                                                                                                                           Query Match 42.4
Best Local Similarity 80.0
Matches 4; Conservative
         ; TOPOLOGY:
US-08-462-661A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 gkgyw 8
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Patent No. 5747447

GENERAL INFORMATION:

APPLICANT: SWIFT, ROBERT L.

APPLICANT: RANDOLPH, ANNE

TITLE OF INVENTION: STABLE POLYPEPTIDE COMPOSITION

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:

ADDRESSE: COOLEY GOOWARD CASTRO HUDDLESON & TATUM

STREET: FIVE Palo Alto

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 1; Length 6;
Pred. No. 1.7e+05;
1; Mismatches 0; Indels
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FILING DATE: 30-APRIL-1993
APPLICATION NUMBER: US 07/876,625
FILING DATE: 30-APRIL-1992
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD L. NEELEY, Ph.D.
REGISTRATION NUMBER: 30,092
REFERENCE/DCOKET NUMBER: CORT-003/08US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUWTRY: USA
ZIP: 94306-2155
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: ASCIT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,661A
FILING DATE: 5-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION: ADATA:
               REGISTRATION NUMBER: 34,297
REFERENCE/DOCKET NUMBER: 2002/001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 425-7200
TELEFAX: (212) 425-5288
TELEX: 440018
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORIGINAL SOURCE:
; ORGANISM: N/A (synthetic)
US-08-232-261-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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TELEFAX: (415)857-0663
Bonham, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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US-08-462-661A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:|
| WGRG 4
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3 wgkgyw 8
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; LENGTH: 8
5318899-41
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APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: DETERSON, JERRY A.
APPLICANT: PETERSON, JERRY A.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
TITLE OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.4%; Score 25; DB 1; Length 8; Best Local Similarity 80.0%; Pred. No. 1.7e+05; Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: /note= "This position is C-NH2." US-08-462-661A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INNORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECHONE: (415) 813-5600
TELEPAN: (415) 494-0792
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD L. NEELEY, Ph.D.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: CORT-003/08US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)843-5000
TELEPEAX: (415)857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/08525539A Patent No. 6309636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site LOCATION: 8
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 gkgyw 8
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US-08-525-539A-39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GKGDW 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-525-539A-39
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Query Match

Best Local Similarity

Qy 3 wgkgyw 8

1 UNGDYW 8

TESULT 15

S13899-41

TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS

TITLE OF INVENTION DATE: US/O7/483,229

FILING DATE: 16-JUN-1989

FILING DATE: 16-JUN-1989

SED ID NO.41:

CUERY MATCH

QUERY MATCH

QUERY MATCH

QUERY MATCH

QY 4 gkgyw 8

QY 4 gkgyw 8

OUGHER OF SECULTS

QY 4 gkgyw 8

Search completed: August 12, 2002, 17:14:59

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August 12, 2002, 17:18:51; Search time 24.99 Seconds (without alignments) 30.761 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                10-071247-2
66
1 cywgcgyw 8
                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                 Scoring table:
                                                                                           Run on:
```

Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

603

Minimum DB seq length: 0 Maximum DB seq length: 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	hypothetical TCL3 gut pentapeptide - T-cell receptor ga acylase - Kluyvera T-cell receptor ga Cadmium-binding he tubulin beta-3 cha T-cell receptor be Rajorensin VI - Ma leucokinin VI - Ma leucokinin VII - T-cell receptor be R-phycoerythrin ga cadmium-blading pe hemoglobin, extrace	
<u>v</u>	179564 JH0253 F41946 F41946 B41948 B41948 B41948 B41948 B410622 P40632 P40632 P40632 P40632 P40632 P40632 P40633 P406331 P406331 P50631 P50	
DB	400000000000000000000000000000000000000	
	60000000000000000000000000000000000000	
Query Match	22.4.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	
Score	10000000000000000000000000000000000000	
Result No.		

ö

Gaps

; 0

Query Match
30.3%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels

6 gyw 8 |:| 1 GFW 3

Q

glycoprotein compo T-cell receptor be	Ig heavy chain CRD cerebellar degener dermorphin (Trans	mabinlin II chain Ig mu chain D regi	globulin I alpha ameletin - rat dermorphin - Rohde	fatty-acid synthas glutathione transf dermorphin (Lys-7) metallothionein is
2 H48394 2 PT0532 2 A58512	2 PT0278 2 B35640 2 S21230	2 S38516 2 E33932 2 A41117	2 S09478 2 A61411 1 A61324	2 A60139 2 S71870 2 S36662 2 S59622
22.7 6 22.7 6	21.2 5 21.2 6 21.2 6	21.2 7 21.2 7 21.2 8	19.7 4 19.7 6 19.7 7	9.7 7 7 19.7 8
115	777	1 1 1 4 4 1	11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	33333
30 31 32	33 34 35	36 37 38	39 4 4 0	4 4 4 4 4 4 4 5

## ALIGNMENTS

RESULT 1 179564 hypothetical TCL3 protein (mistranslated) - human (fragment) C;Species: Homo sapiens (man) C;Decies: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000 C;Accession: 179564 R;Zutter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.: Morfon. C.
Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990 A,Title: The t(10:14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the A;Reference number: 159162; MUID:90222189 A;Accession: 179564
A;Status: translation not shown; translated from GB/EMBL/DDBJ A;Molecule type: DMA A;Residues: 16 < ZUT> A;Cross-references: GR:M33602: NID-G330007: DIDN:AAA66440 1: DID.GOODEE
C;Comment: This is the hypothetical translation of a sequence translated in an incorr
Query Match 34.8%; Score 23; DB 4; Length 6; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 wgcg 6
Db 2 WCcG 5
RESULT 2 JH0253
gut pentapeptide - Japanese eel C;Species: Anguilla japonica (Japanese eel)
<pre>C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995 C:Accession: JH0253</pre>
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M. Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A, Title: Structure and function of a pentapeptide isolated from the gut of the eel. A, Reference number: JH0253; MUD:92062113 A:Accession: JH0253
A;Molecule type: protein A;Residues: 1-5 <ues. A;Rxperimental source: gut</ues. 
C;Comment: This peptide increased basal tone of the circular muscle of the esophagoga, and of the circular muscle of the gastro-intestinal junction.

a

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T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Specias: Oryctolagus cuniculus (domestic rabbit)
C;Specias: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity an A;Reference number: A53284; MUID:91342695
A;Accession: B53284
A;Actus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                    cadmium-binding heptapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C;Accession: B33882
R;Jackson, P.J.; Unkefer, C.J.; Dooll-, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan A;Reference number: A94182; MUID:88016144
A;Accession: B33882
A;Molecule type: protein
A;Residues: 1-7 <JA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)

(Species: Drosophila melanogaster

(Spacession: S33567

(Shacession: S33567

(Share: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000

(Shacession: S33567

(Share: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000

(Shacession: S33567

(Share: Nork, A.): Renkantiz-Pohl, R.

(Share: Development 116, 543-554, 1992

(Share: Development 116, 543-554, 1992

(Share: Driving S33567; MUD: 93170162

(Share: Share: Drelininary; translation not shown

(Share: Drelininary; Translation not shown)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g4377448 C;Genetics: A;Gene: F;Ygase:sbgr A;Gene:Fygase:sbgr A;Cross-references: FlyBase:Fbgn0003888 A;Introns: 5/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%; Score 18; DB 2; 1 50.0%; Pred. No. 2.8e+05; tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 18; DB 2; 140.0%; Pred. No. 2.8e+05; iive 1; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.3
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CECECG 7
2 ywgcgy 7
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                                                                 1 YRGSGF
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A41946
T-cell receptor gamma chain (1t.22) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
R;Motssell, M.: Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946
A;Residues: preliminary; not compared with conceptual translation
A;Residues: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                    Ryhetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
Aprille: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge A; Reference number: A41946; MUID:92049316
A; Accession: F41946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Xluyvera cryocrescens
C.Species: Xluyvera cryocrescens
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C.Accession: 519288
R.Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A.Feference number: 519288; MUID:92109664
A.Accession: 519288
A.Accession: 519288
A.Accession: Supplementy
A.Molecule type: protein
A.Residues: 1-8 <AAR>
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                                                                                                                                             C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 2; Length 6;
Pred. No. 2.8e+05;
0; Mismatches 2; Indels
                                                                                                            T-cell receptor gamma chain (la.27) - mouse (fragment)
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity
Matches 2; Conserv
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Cipacies: Psychrobacter immobilis
Cipate: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
Cipate: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
Ciaccession: S57274
Riaption, J.L.; Feller, G.; Gerday, C.
Biochim. Biophys. Acta 1263, 103, 1995
A;Fitle: Corrigendum to "Cloning, sequence and structural features of a lipase from t
A;Recession: S57274
A;Accession: S57274
A;Accession: S57274
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                cell receptor beta chains have few N regions
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J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0509; MUID:91277601
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                                                                  Treel1 receptor beta chain V-D-J region (111-1K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: PT0637
R;Feeney, A.J.
J. Exp. Med. 174, 1991
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few A;Reference number: PT0639
A;Fitle: Junctional sequences of sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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A; Cross-references: EMBL:X67712
C; Keywords: carboxylic ester hydrolase
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A,Molecule type: mRNA
A,Residues: 1-7 <FEE>
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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J. Exp. Med. 174, 115-124, 1991
A; Title: Juncitional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
A; Accession: PT0629
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A61068
A61068
A61068
G.Species: Locusta migratory locust
C.Species: Locusta migratory locust
C.Species: Locusta migratoria (migratory locust)
C.Species: Joec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C.Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A. Regul. Pept. 37, 49-57, 1992
A; File: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, A; Reference number: A61068; MUID:92262851
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
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A;Residues: 1-6 <SCH>
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental
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                           A;Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:9233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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A) Status: translation not shown
A) Molecule type: mRNA
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A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                     0; Indels
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25.8%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                   Length 4;
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                                                                                                                                                                                               25.8%; Score 17; DB 2; Le
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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Pred. No. 2.8e+05;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pr
Matches 2; Conservative 0;
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
                                                                                                                                                                                            Query Match 25.88
Best Local Similarity 100.0
Matches 2; Conservative
A; Residues: 1-4 <HAR>
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PRESULT 15
Pr0722
T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: Pr0722
B; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Recence number: Pr0509; MUID:91277601
A; Accession: Pr0722
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-7 < FEE>
A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
                                                                                                                                                                                                                             Cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 17-ul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0642
A; Titler Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
A; Accession: PT0642
A; Status: translation not shown
A; Mesidues: 1-7 < FEE>
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A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0; Indels
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August 12, 2002, 17:20:43 ; Search time 13.13 Seconds (without alignments) 23:592 Million cell updates/sec
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-1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINGUT).
-1- SIMILARITY: TO THE OPHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holman G.M., Cook B.J., Nachman R.J.; "Isolation, prinary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
                                                        Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura 'Isolation of angiotensin-converting enzyme inhibitor from tuna
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8 AA; 893 MW; DC6365B449CDC76A CRC64;
                                                                                                           muscle.",
Blochem. 155:332-337(1988).
Blochem. 155:332-337(1988).
PIR. 371570; A31570.
SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 18, Created)
(Rel. 18, Last sequence update)
(Rel. 18, Last annotation update)
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NCBI_TaxID=6988;
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                             MEDLINE-88326322; PubMed-3415688;
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MOD_RES 8 8
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 2; Conservative
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SEQUENCE, AND SYNTHESIS.
TISSUE=Head;
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Matches 2; Conserv
TISSUE-Muscle;
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01-MAY-1991 (
01-MAY-1991 (
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P21140;
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LCK1_LEUMA
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LCK2_LEUMA
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Holman G.M., Cook B.J., Nachman R.J.;

"Isolation, primary structure and synthesis of two neuropeptides from Leucophaca maderae: members of a new family of cephalomyotropins.";

Comp. Biochem. Physiol. 84C:205-211(1986).

-i. FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE

-i. SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holman G.M., Cook B.J., Nachman R.J.; "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin III (L-III).
Leucophaea maderae (Madeira cockroach).
Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota: Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.
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01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin IV (L-IV).
Leucophaea maderea (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
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MOD_RES 8 8 AMIDATION.

SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;
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100.0%; Pred. No. 1e+05;
tive 0; Mismatches 0
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                                                                                                                                                                                                            Neuropeptide; Amidation.
MOD_RES 8 8
SEQUENCE 8 AA; 852 MW;
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Best Local Similarity
These 2; Conservat
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Matches 2; Conserv
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MEDLINE-8702551; Pubmed-2877794;
MEDLINE-8702551; Pubmed-2877794;
MEDLINE-8702551; Pubmed-2877794;

"Isolation, primary structure, and synthesis of leucokinins V and VI:
"Isolation, primary structure, and synthesis of leucokinins V and VI:
"Isolation, primary structure, and synthesis of leucokinins V and VI:
"Isolation, primary structure, and synthesis of leucokinins V and VI:
"Isolation Physiol. 88C:27-30(1987).
"Isolation Physiol. 88C:27-30(1987).
"Isolation: Physiol. 88C:27-30(1987).
"Isolation Physiol. 88C:27-30(1987).
"Isolation Physiol. BREATH AND TO MANDUCA SEXTA AND REIN, JS0316; JS0316.
"In PARROLIDONE CARBOXYLIC ACID.
"MOD_RES I B MAIDATION.
"SEQUENCE 8 AA, 935 MW; 9D636581E9DSASA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of leucokinins VII and VIII the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:31-34(1987).
--- FUNCTIONIC SCEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
--- SIMILARITY: TO THE OTHER LEUCOKININS.
--- SIMILARITY: TO THE OTHER LEUCOKININS.
       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Orthopteroldea; Dictyoptera; Blattaria;
Blaberoldea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VII (L-VII).
Leucokinin VII (L-VII).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; NCBL_TaxID-6988;
                                                                                                                                                                                                                                                                                                                                            0; Indels
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DC6365A5B9CDC76A CRC64;
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                                                                                                           STIMULATES CONTRACTILE
                                     Holman G.M., Cook B.J., Nachman R.J.;
"Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
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Leucokinin V (L-V).
Leucophaea maderae (Madeira cockroach).
Leucophaea maderae, Arthropoda; Tracheata; Hexapoda; Insecta;
Pletygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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Pred. No. 1e+05;
0; Mismatches 0; Indels
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8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;
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100.0%; Pred. No. 1e+05;
tive 0; Mismatches (
                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Leucokinin VI (L-VI).
Leucokhaea maderae (Madeira cockroach).
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               SEQUENCE, AND SYNTHESIS.
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les 2; Conserv
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P19987;
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"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
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                                                                                                                                                            Holman G.M., Cook B.J., Nachman R.J.;

"Isolation, primary structure and synthesis of leucokinins VII and
"Isolation, primary structure and synthesis of leucokinins VII and
VII: the final members of this new family of cephalomyotropic
peptides isolated from head extracts of Leucophaea maderae.";

Comp. Biochem. Physiol. 88C:31.34(1987).

-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-!- SIMILARITY: TO THE OTHER LEUCOKININS.

PIR; JS0318; JS0318.

Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                OCTOMIC STANDARD; PRT; 4 AA.
PS8649;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
Cardioactive peptides Ocp-3/Ocp-4.
Cardioactive Mollusca; Cephalopoda; Coleoidea; Octopoda; Incirrate; Octopodidae; Octopous.
                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides 21:623-630(2000).
-!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-4 is a 1000 time less
                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
NCBL_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.7%; Score 15; DB 1; Length 4; 66.7%; Pred. No. 1e+05; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                             Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 2 D-SERINE (IN OCP-4).
4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                 8 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
                                                                                                                                                                                                                                                                                                                            25.8%; Score 17; DB 1;
100.0%; Pred. No. 1e+05;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: Mw=395.2; METHOD=MALDI.
                      (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 17, Last annotation update)
8 AA.
                                                        Leucokinin VIII (L-VIII).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              active than Ocp-3.
SUBCELLULAR LOCATION: Secreted.
 PRT;
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 STANDARD;
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Best Local Similarity
2; Conserve
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Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10876044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                   TISSUE=Head;
                      01-FEB-1991
                                             01-FEB-1991
                                  01-FEB-1991
 LCK8_LEUMA
P19990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; D
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                              TISSUE-Fibroblast;
MEDLINE-95009907; PubMed-7523108;
MEDLINE-95009907; PubMed-7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: ON THE 2D-CEL THE DETERMINED PI OF THIS UNKNOWN PR.
NON TER.
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A., "Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).

-1 - SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                              Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.7%; Score 15; DB 1; Length 5; 66.7%; Pred. No. 1e+05; ive 0; Mismatches 1; Indels
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898 MW; 922879CABB58640D CRC64;
                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 5.
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5 AA.
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PRT;
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MEDLINE=98054539; PubMed=9392829;
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3 GY
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-1- FUNCTION: THE PEPTIDE PERTIDE HORMONE INDUCES GALL BLADDER CONTRACTION AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION IN THE BRAIN IS NOT CLEAR.

-1- SIMILIARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

PIR; PQ0012; PQ0012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting enzyme inhibitor).
Bothrops insularis (Island jararaca) (Queimada jararaca).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
                                                                                                       Macropus eugenii (Tammar wallaby), and Dasyurus viverrinus (Southeastern quoll). Bukaryota: Metacasa: Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Metatheria: Diprotodontia; Macropodidae; Macropus. NCBI_TaxID=9315, 9279;
                                                                                                                                                                                                                     Fan Z.W., Eng J., Shaw G., Yalow R.S.; "Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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DDCAA68378768B5A CRC64;
                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-COT-1996 (Rel. 34, Last annotation update)
Cholecystokinin (CCK).
                        8 AA.
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                         PRT;
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                                                                                                                                                                              SEQUENCE.
TISSUB-Brain;
MEDLINE-88234141; PubMed-3375140;
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PROSITE: PSO0259; GASTRIN; 1.
Amidation; Sulfation; Hormone.
MOD_RES 8 8 A
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ilarity 66.7%;
Conservative
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                        STANDARD;
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2; Conserv
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BPP7_BOTIN
ID BPP7_BOTIN
AC P30425;
                        CCKN_MACEU
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SEQUENCE.
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                                 P30369;
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          CCKN_MACEU
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                              1 1 PYRROLIDONE CARBOXYLIC ACID. 5 AA; 629 MW; 776DC37326B00000 CRC64;
                                                                                   16.7%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 1e+05; 1ve 0; Mismatches 0; Indels
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Job time: 340 sec
             Hypotensive agent; Venom.
MOD_RES 1 1
SEQUENCE 5 AA; 629 MW;
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PIR; G37196; G37196
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Best Local Similarity
Matches 1; Conserv
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Q96rn9 homo sapien
Q64971 alfalfa mos
Q9r5r2 shigella dy
Q95213 oxyctolagus
P82096 litoria rub
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choloepus h
choloepus d
euphractus
                                                                                                                                                                     condylura c
sorex arane
echinops te
trichechus
                                    Q95945 saccharomyc
P82065 litoria rub
                                                                                                                                                myrmecophag
erinaceus c
talpa altai
                                                                        homo sapien
drosophila
                                                                                       sus sp. ins
didelphis m
                                                    synechococc
                                                          coxiella bu
                                                                  homo sapien
                                                                                                                                          tamandua te
                                                                                                                                                                                                   procavia ca
loxodonta a
                                                                                                                                                                                                                                                                                                                                                                     Vuorio E.;
"Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996).
EMBL; S83371; AAD14433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                       002831;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Lagomorpha; Leporidae; Oryctolagus.
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                                                                 Q9byy5
Q15888
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MEDLINE-96377339; PubMed-8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 6; Length 8;
Pred. No. 5.6e+05;
1; Mismatches 1; Indels
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8 AA; 1028 MW; B859C7272EA77371 CRC64;
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Q9BFB0
Q9BFA9
Q9BFA8
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30.3%;
50.0%;
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 Query Match
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Matches 2; Conserv
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SEQUENCE
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                 protein search, using sw model
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Q9YIQ0
Q15890
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Gapop 10.0 , Gapext 0.5
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sp_fungi:*
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Match Length
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(TrEMBLrel. 06, Created)

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TISSUB-CORPORA CARDIACA,
MEDINDE-98010462; PubMed-9350979;
Predel R., Kalner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the
retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                         KININ-2 (PEA-K-2).

Periplaneta americana (American cockroach).

Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,

Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria,

Blattoidea, Blattidae, Periplaneta.

NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KININ'3 (PEA-K-3).
Periplaneta americana (American cockroach).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Petrygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattcidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEGUL. PEPt. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                               americana.";
Regul. Pept. 71:199-205(1997).
-!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
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Last annotation update)
                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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8 AA; 909 MW; DC6365B449D5A76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.8%; Score 17; DB 5; L 100.0%; Pred. No. 5.6e+05;
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Pred. No. 5.6e+05;
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (MYOTROPIC ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION
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                                                                                          Created)
                                                      PRT;
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MEDLINE-98010462; Pubmed-9350979;
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                                                                                        (TrEMBLrel. 16,
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MOD_RES 8 8
SEQUENCE 8 AA; 856 MW;
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                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                     SEQUENCE, AND FUNCTION.
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Best Local Similarity
'-has 2; Conserva
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                                                                                        01-MAR-2001
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SEQUENCE
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P82687;
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P82686
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                                           Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I: Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

NCBI_TaxID=3847;
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TISSUE-CORPORA CARDIACA;

MEDLINE-98010462; Pubmed-9350979;

Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;

Tisolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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01-MAR-2001 (TTEMBLrel. 16, Last sequence update)
01-MAR-2001 (TTEMBLrel. 16, Last annotation update)
01-MAR-2010 (TTEMBLrel. 16, Last annotation update)
NININ-1 (PRA-K-1).
Periplaneta americana (American cockroach).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Petryyota, Neoptera, Orthopteroidea, Dictyoptera, Blattaida, Noblatidae, Periplaneta.
NCBI_TAXID-6978;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 10; Length 7; Pred. No. 5.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
STRAIN-CV. ESSEX; TISSUE-ROOT;
Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1; -.
01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HMG-1-LIKE PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA; 850 MW; 6AAAAB378637810 CRC64;
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100.0%; Pre
0; }
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CV. ESSEX; TISSUE-ROOT;
MEDLINE-91367679; PubMed~1891369;
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MOD_RES 8 8
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Best Local Similarity
Matches 2; Conserva
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Best Local Similarity
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Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
"Small subunit of the mammalian mitochondrial ribosome. Identification
of the full complement ribosomal proteins present.";
Submitted (DEC-2000) to the SWISS-PROT data bank.
-! SUBCELLULAR LOCATION: MITOCHONDRIAL.
Ribosomal protein; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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STRAIN-KN T96-0620, S-1058, AND CL 68578;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
Crawford-miksza L.K., Nang R.N., Schnurr D.P.;
Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitteed (MAX-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065068; AAD03668.1;
EMBL; AF065066; AAD03668.1;
EMBL; AF065067; AAD03666.1;
EMBL.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=85755;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bovidae; Bovinee; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

MCBI_TaxID=9913;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) (FRAGMENT).
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Last annotation update)
             C76365B449CDC775 CRC64;
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                                                                      25.8%; Score 17; DB 5; Lo 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0;
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100.0%; Pred. No. 5.6e+05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          8 AA.
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             865 MW;
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
'-haq 2; Conserve
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les 2; Conserv
             8 AA;
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Best Local S
Matches 2
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Q9YIRO;
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P82929;
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MEDLINE-98010462; PubMed=9350979;
Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
Prolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-5 (PEA-K-5).
Periplaneta americana (American cockroach).
Periplaneta americana (American Cockroach).
Periplaneta mericana; Orthopteroidea; Insecta; Periplaneta; Orthopteroidea; Dictyoptera; Blattaidae; Periplaneta.
NOBI_TAXID-6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regul. Pept. 71:199-205(1997).
-I-FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-I-SIMILARITY: BELONGS TO THE KININ FAMILY.
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-1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-1- SIMILARITY: BELONGS TO THE KININ FAMILY.
Neuropeptide; Amidation.
MOD_RES
        Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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8 AA; 839 MW; 736365A5B9D6DDD8 CRC64;
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  Mismatches
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  ;
    Conservative
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                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
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MEDILINE=21429115; PubMed=11543634;
MEDILINE=21429115; PubMed=11543634;
Kennaochi N., Suzuki T.,
Watanaochi N., Tanaka T.;
"The human mitochondrial ribosomal protein genes: Mapping of 54 get to the chromosomes and implications for human disorders.";
Genomics 77:65-70(2001).
EMBL; AB051346; BAB54936.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(CLONE XP19G12A) (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL; L32083; AAA73880.1; -.
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              24.2%; Score 16; DB 12; Length 7; 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOGHONDRIAL RIBOSOMAL PROTEIN L39 (FRAGMENT).
MRPL39.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBL_TaxID=28280;
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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MEDLINE-99175282; PubMed=10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Strain variation in adenovirus serotypes 4 and 7a causing acute
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065065; AAD03662.1; -.
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SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PVI CORE PROTEIN (FRAGMENT).
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24.2%; Score 16; DB 12; I 100.0%; Pred. No. 5.6e+05; ive 0; Mismatches 0;
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J. Clin. Microbiol. 37:1107-1112(1999).
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Q1-MAX-1999 (TEMBLEE]. 10, Li

Q1-OCT-2001 (TEMBLEE]. 18, L.

PVI CORE PROTEIN (FRAGMENT).
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=96198747; PubMed=8612486;
YOShikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-ROOT;
MEDLINE-21171025; PubMed-11277426;
Wercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
Arabidopsis Indiana genes expressed in the early compatible interaction with root-knot nematodes.";
Mol. Plant Microbe Interact. 14:288-299(2001).
EMBL; AJ286350; CAB71014.2; -...
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 0.7 KDA PROTEIN (FRAGMENT).
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                                                      14.2%; Score 16; DB 4; Lo ilarity 100.0%; Pred. No. 5.6e+05; Conservative 0; Mismatches 0;
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
ORPHAN RECEPTOR TR4-NS (FRAGMENT).
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Endocrinology 137:1562-1571(1996).
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Gaps
                                                   Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.; "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene."; Genomics 35:361-366(1996).

EMBL; U59454; AAB914331; ...
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7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-96299786; Pubmed-8661150;
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Neuromedin B and s
Immunogenic peptid
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(F-18)
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                                                                                                                    Search time 48.76 Seconds (without alignments) 18.224 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuromedin B
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Fluorine-18
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version 4.5
- 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                   747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                    August 12, 2002, 17:14:32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100%
first 45 summaries
                                                                             protein search, using sw model
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AAY76817
AAY03714
AAY03716
AAY42915
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AAB59640
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-terminal acetylation; optionally has a free or protected thiol group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       optionally has a free group"
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protected thiol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "D-form residue"
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                                                               AAW50949
AAW45748
AAX42906
AAX42910
AAX42910
AAX42910
AAX42913
AAX42919
AAX2919
AAX2919
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AAX5919
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AAX5919
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AAU08872
AAB59629
AAB59630
AAB59631
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AAB59645
AAB91376
AAB59642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fluorine-18 (F-18) labeled peptide 2.
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  AAY03715 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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RESULT
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11-MAR-1999

Biostatin TT232 sy

/note= "D-form residue"

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Misc-difference
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                                                                                                                                                                                                                                                                                                                                              conjugates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                          The invention relates to a method for incorporating 18F radionuclide into peptide-containing targeting vectors for use in clinical positron emission temporaphy. Radiolabeling thiol-containing peptides with canisation temporaphy. Radiolabeling thiol-containing peptides with canisation temporaphy. Radiolabeling thiol-containing a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CRIR2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon abears at least one leaving group comprising 1. Br. Cl. azide, tosylate, mesylate, nosylate, n. m = 0-2; n.m = 0-2; x = 1, Br. Cl. azide, tosylate, mesylate, nosylate, triflate, maleimide of principally substituted by 1-2 alkyl) or 3-sulfomaleimide; Rl. R2 = I, Br. Cl. azide, terriary amine, quaternary ammonium, alkyl. Br. Cl. azide, terriary amine, quaternary ammonium, alkyl. OOK, COOK, OOK, OK) of sulfonic acid, terliary amine or quaternary ammonium, cook, terriary amine, quaternary ammonium, alkyl. COOK, cook; of coptionally substituted by CONH2, COOH, OH, sulfonic acid, terliary amine or quaternary ammonium, cook, sulfonic acid, terriary amine or quaternary ammonium, alkyl. COOK, cook; on the containing vectors such as proteins, antibodies, antibody fragments and receptor-targeted peptides for Radiolabeling peptide-containing receptor-targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY0314-716 represent examples of F-18 labeled peptides used in the method of detecting a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
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                                                                                                                                           Radiolabeling thiol-containing peptides with fluorine-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 66; DB 20; 100.0%; Pred. No. 6.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY76817 standard; peptide; 8 AA.
                                                                                                                                                                      Claim 14; Page 15; 22pp; English.
            98WO-US18268
                                     97US-0057485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                IMMU-) IMMUNOMEDICS INC
                                                                                                                  WPI; 1999-228967/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                         Griffiths GL;
                                     03-SEP-1997;
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           03-SEP-1998;
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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprisable administering a bi-specific cartibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targetling methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
"D-form residue; modified with free amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                   protected amino acid group, chelating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                agent or a metal-chelate complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leung S, McBride WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 66; DB 21;
100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                             /note= "D-form residue"
                                                                                                                                        'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fluorine-18 (F-18) labeled peptide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY03714 standard; peptide; 8 AA
                                       group,
                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US13879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0090142.
98US-0104156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-160561/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                    Misc-difference 7
                                                                                                                                                                         Misc-difference 8
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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.

Fluorine-18 (F-18) labeled peptide 3.

(first entry)

08-JUN-1999

AAY03716;

/note= "D-form residue; optionally acetylated"

'note= "D-form residue; D-iodo-Tyr"

/note= "D-form residue"

Misc-difference 8

WO9911590-A1 11-MAR-1999 98WO-US18268,

03-SEP-1998;

(IMMU-) IMMUNOMEDICS INC.

WPI; 1999-228967/19.

3riffiths GL;

'note= "D-form residue; D-iodo-Tyr"

'note= "D-form residue"

Misc-difference 5

Misc-difference

/note= "N-terminal acetylation"

Misc-difference Misc-difference

Modified-site

Synthetic

Location/Qualifiers

m

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The peptide-containing targeting vectors for use in clinical positron containing transcribed to the containing peptides with the labeling reagent of formula is Rev. (CAD)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CRAR2-(CH2)m-CR
                                                                                                                                                                                                                'D-form residue; optionally has a free or
protected amino acid group"
                                            /note= "optionally has a free or protected
   amino acid group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a method for incorporating 18F
                                                                                                                  "D-form residue"
                                                                                                                                                                                                                                                                                   "D-form residue"
                                                                                                                                                              "D-form residue"
                                                                                                                                                                                                                                                                                                                                /note= "D-form residue"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 15; 22pp; English.
                                                                                                                                                                                                              /note= "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US18268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMUNOMEDICS INC.
                                                                                                                    note=
                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                        "note=
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Key
Misc-difference 1
                                                                                         Misc-difference 2
                                                                                                                                                                                                                                                          Misc-difference 7
                                                                                                                                        Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA;
                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths GL;
                                                                                                                                                                                                                                                                                                                                                                               WO9911590-A1
                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1999
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Radiolabeling thiol-containing peptides with fluorine-18

Claim 15; Page 15; 22pp; English.

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into peptide containing targeting vectors for use in clinical positron emission tomography. Radiolabeling thiol-containing peptides with fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRIRZ-(CH2)m-CRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       targeting vectors such as proteins, antibodies, antibody fragments and receptor- targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY0314-716 represent examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for incorporating 18F radionuclide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.2%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenyl. The methoutargeting vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 20; Length 8;
Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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Best\_Local Similarity Matches 6; Conserv

Query Match

||| ||| 2 ywgkgyw 8 2 ywgcgyw 8

à g AAY03716 ID AAY0: XX

20-DEC-1999

AAY42908;

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ò g

AAX42908 RESULT

Synthetic

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The invention relates to the use of certain heptapeptide somatostatin derivatives and/or phenylhydrazone derivatives for the preparation of medicaments possessing neurogenic and/or non-neurogenic antinflammatory and/or analgesic effects. The derivatives are used for treating pain and for treating neurogenic inflammation in the pathomechanism of rhinitis, bronchitis, bronchial asthma, arthritis, allergic conjunctivitis, urticaria, colitis and psoriasis. The present sequence is a preferred example of a heptapeptide somatostatin derivative for use in the invention.
                                                                                                                                                 Somatostatin derivative VZ-1038 for antiinflammatory or analgesic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of somatostatin derivatives and phenylhydrazone derivatives for preparation of medicaments with neurogenic and/or non-neurogenic antiinflammatory and/or analgesic effects -
                                                                                                                                                                            Somatostatin, antiinflammatory; analgesic; rhinitis; bronchitis; bronchial asthma; arthritis; allergic conjunctivitis; urticaria; colitis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helyes Z, Erchegyi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 20; Length 7;
Pred. No. 6.4e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOS-) BIOSTATIN GYOGYSZERKUTATO-FEJLESZTO KFT
                                                                                                                                                                                                                                                                                                                                                                         'note≈ "D-form residue"
                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Szolcsanyi J, Pinter E,
I, Teplan I, Orfi L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59639 standard; Peptide; 8 AA.
                                    AAY42915 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 13; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Gly-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.6%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-0107392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98HU-0000970
                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                     Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA;
                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond Modified-site
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||| ||
2 cywkcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-1998;
                                                                                                                20-DEC-1999
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Horvath J,
                                                                                                                                                                                                                                                               Synthetic
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                                                                           AAY42915;
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 RESULT
AAY42915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the use of certain heptapeptide somatostatin derivatives and/or phenylhydrazone derivatives for the preparation of medicaments possessing neurogenic and/or non-neurogenic antiinflammatory and/or analgesic effects. The derivatives are used for treating pain and for treating neurogenic inflammation in the pathomechanism of rhinitis, bronchitis, bronchial asthma, arthritis, allergic conjunctivitis, urticaria, colitis and psoriasis. The present sequence is a preferred example of a heptapeptide somatostatin derivative for use in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helyes 2, Erchegyi J, Horvath A;
                                                                                                                                                                                                                                           Somatostatin derivative VZ-934 for antiinflammatory or analgesic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of somatostatin derivatives and phenylhydrazone derivatives for preparation of medicaments with neurogenic and/or non-neurogenic antiinflammatory and/or analgesic effects -
                                                                                                                                                                                                                                                                          Somatostatin; antiinflammatory; analgesic; rhinitis; bronchitis; bronchial asthma; arthritis; allergic conjunctivitis; urticaria; colitis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 42; DB 20; Length 7; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOS-) BIOSTATIN GYOGYSZERKUTATO-FEJLESZTO KFT.
                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Szolcsanyi J, Pinter E,
                                                                                                                               AAY42908 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Thr-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 13; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orfi L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-0107392.
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                                                                                                                                                                                                         (first entry)
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Best Local Similarity 100.
Matches 5; Conservative
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EP952159-A2 27-0CT-1999 Horvath J,

Keri G,

NAME OF THE PROPERTY OF THE PR

Horvath A;

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Gaps

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Sequence

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Length 7;

AAB59640 standard; Peptide; 8 AA.

RESULT AAB59640

(first entry)

23-MAR-2001

AAB59640;

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(WMB). These can be used in the treatment of various cancers, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic solerosis, external and internal pancreatic pseudocysts and ascites, nesidoblastosis, irritable bowel syndrome, pancreatitis, amall bowel obstruction, pastrooesophageal reflux, duddenogastric reflux, cushing's syndrome, hyperparathyroidism, Graves' disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, orthostatic hypotension, postprandial hypotension, panic attacks, diabetes mellitus, hyperlipidaemia, insulin insensitivity, syndrome X, peptic ulcers, arthritis, obesity, opioid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention provides analogues of somatostatin and neuromedin B
                                                                     Neuromedin B; NMB; somatostatin; analogue; Helicobacter pylori; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide compounds are somatostatin and neuromedin B receptor agonists, for treating a wide range of disorders e.g. cancer, gastrointestinal disorders and inflammatory disorders -
                                                                                                                                                                                                               'note= "disulfide bond cyclises the peptide"
                                                                                                                                                                                    'note= "modified by D-4-NO2"
                                          Neuromedin B and somatostatin analogue #32.
                                                                                                                                                                                                                                                                                                                                              /label= OTHER
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                    /label= OTHER
/note= "modified by Bzl"
                                                                                                                                                                                                                                             'note= "D-form residue"
                                                                                                                                                                                                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overdose and gastrointestinal bleeding.
                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                       /label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sadat-Aalaee D, Morgan BA;
                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOM-) BIOMEASURE INC
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               23-MAR-2001
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                                                                                                               Synthetic.
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                                                                                     cyclic.
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(NMB). These can be used in the treatment of various cancers, anorexia, hypothyroidism, hyperaldosteronism, Helicobacter pylori proliferation, acromegaly, restenosis, Crohn's disease, systemic solerosis, external and internal pancreatic pseudocysts and ascites, nesidoblascosis, hyperinsulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma, hyperinsulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma, gastrooesophageal reflux, duodenogastric reflux, Cushing's syndrome, hyperparathyroidism, Graves' disease, diabetic neuropathy, Paget's disease, polycystic ovary disease, orthostatic hypotension, postprandial hypotension, panic attacks, diabetes mellitus, hyperlipidaemia, insulin insensitivity, syndrome X, peptic ulcers, arthritis, obesity, opioid overdose and gastrointestinal bleeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides analogues of somatostatin and neuromedin B
                                                                                                    Neuromedin B; NMB; somatostatin; analogue; Helicobacter pylori; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide compounds are somatostatin and neuromedin B receptor agonists, for treating a wide range of disorders e.g. cancer, gastrointestinal disorders and inflammatory disorders
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                                                                                                                                                                                                         /label- OTHER
/note= "N-(2-aminoethyl)-N-(2-thyminyl-1-oxo-ethyl)
-glycine"
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                                                                                                                                                                                                                                                                 note= "disulfide bond cyclises the peptide"
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Pred. No. 6.4e+05;
0; Mismatches 2; Indels
                                                                          Neuromedin B and somatostatin analogue #33.
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                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                /note= "D-form residue"
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
/note= "modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 73; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       /label= OTHER
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sadat-Aalaee D, Morgan BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOM-) BIOMEASURE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-146787/15.
                                                                                                                                                                                                                                                                                 Misc-difference
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Modified-site
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                                                                                                                                                  Synthetic.
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Length 8;

Score 39; DB 22; Length 8; Pred. No. 6.4e+05; 0; Mismatches 2; Indels

59.1%; 71.4%;

Conservative

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Query Match Best Local Similarity Matches 5; Conserv

Length 8;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating a bi-specific diseased tissues in a patient comprising administering a bi-specific attibudy (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds targeted conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                       Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                               Immunogenic peptide for bi-specific antibody recognition.
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                                                                                                                                                                                                                                                                                                                                                                                         note= "acetylated D-form residue"
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                                                                                                                                                                                                                                                                                                                                   'note= "D-form iodo-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "D-form lodo-Tyr"
                                                                                                                                                                                                                                                                                                                                                               note= "D-form residue"
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                                                                                                                                                                                                                                                                                                         'note= "acetylated"
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                                                                                              AAY76818 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0090142.
98US-0104156.
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                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUNOMEDICS INC
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                                                                                                                                                                                                                                                     Synthetic.
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Sequence

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                                                                                                                                                                                                                                                      Neuromedin B; NMB; somatostatin; analogue; Helicobacter pylori; cancer;
                                                                                                                                                                                                                                                                                                                                                          /note= "optionally N-(3-indolylacetyl)-L-phenylalanine,
                                                                                                                                                                                                                                                                                                                                                                     N-(2-aminoethyl)-N-(2-thyminyl-1-oxo-ethyl) glycine, N-(2-aminoethyl)-N-(2-cytosinyl-1-oxo-ethyl)-glycine, 5-(4-methyl-2-nitrophenyl)-2-furoic acid,
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "disulfide bond cyclises the peptide"
                                  Indels
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DB 21; Leu. 6.4e+05;
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                              Mismatches
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/note= "C-terminal amide"
        Score 37; 1
Pred. No. 6.
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/note= "modified by Bzl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "D-form residue"
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                                                                                                                                                     AAB59641 standard; Peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                /label= OTHER
          56.1%;
71.4%;
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                                                                                                                                                                                                       (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "note=
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                      Best Local Similarity
Matches 5; Conserv
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Gaps

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Length 6; 1; Indels

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while still bonded to the solid phase. The products of the invention have cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits and the tyrosine kinase activity of various human stoomach cancer cell lines and thus inhibits cellular proliferation. The heptapeptide (I) described in the invention is a somatostatin analog which shows strong antitumor eativity in vitro and in vivo. The SP synthesis method gives (I) is more which the cyclization is carried out after cleaving the peptide from the which the cyclization method is also a simple synthesis of (I) in high yield; typically the tert-butyl-protected precursor can be oxidized in a yield of 70-80%. Ax51896-x51900 represent peptides used in the synthesis of biostatin T7232 described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; cancer; neoplasm; malignancy; psoriasis; regulation of; release of; growth hormone; insulin; glucagon; prolactin; inhibit exopeptidase; inhibit tumour growth; tumour transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Bokonyi G, Csuka O, Horvath A, Horvath J, Idei M;
Mezoe I, Seprodi J, Szoke B, Teplan I, Vadasz Z;
I G, Seproedi J, Szoeke B, Mezo I, Templan I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New octa:peptide or hepta:peptide somastatin analogues - as tyrosine kinase inhibitors for treating tumours and psoriasis, and for regulating hormone release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatostatin analogue tyrosine kinase inhibitor #3.
                                                                                                                                                                                                                                        Score 34; DB 21;
Pred. No. 6.4e+05;
                                                                                                                                                                                                                                                                     Mismatches
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(BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 AAR27179 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "D-form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "D-form"
                                                                                                                                                                                                                                       51.5%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                              6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_d1fference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disulfide_bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified_site
                                                                                                                                                                                                                                                                                                                  Cywkc 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keri<sup>G</sup>, Mezoo
Boekoenyi G,
                                                                                                                                                                                                                                                                                                cywgc 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Balogh A,
                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR27179;
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                                                                                                                                                                                                                                                                                                                                                                                    AAR27179
          222222222222222
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hyperinsulinism, Zollinger-Ellison syndrome, diarrhoea, scleroderma, irritable bowel syndrome, pancreatitis, small bowel obstruction, gastrooesophageal reflux, duodenogastric reflux, cushingy s syndrome, hyperparathyroidism, Graves' disease, diabetic neuropathy, paget's disease, polycystic ovary disease, orthostatic hypotension, panic attacks, diabetes mellitus, hyperinjidaemia, insulin insensitivity, syndrome X, peptic ulcers, arthritis, obesity, oploid overdose and gastrointestinal bleeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for the solid phase (SP) synthesis of biostatin (TT 232) (I) which includes closing the disulfide bridge by oxidation of the completely or partially constructed peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor; cellular proliferation inhibition; somatostatin; antitumor.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biostatin preparation in high yleld by solid synthesis, including closure of disulfide bridge before cleavage from support, useful
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Thr(tBu) with C-terminal amide group"
                                                                                                                                                                         Score 35; DB 22; Length 8;
Pred. No. 6.4e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.
                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Biostatin TT232 synthesising peptide 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Ddz-Cys(Acm)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Tyr-(tBu)"
                                                                                                                                                                                                                                                                                                                                  AAY51899 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Cys(Acm)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 25; 33pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Lys(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birr C;
                                                                                                                                                                           53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-EP06131.
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braum G, Lifferth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-224663/19.
                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antitumor agent -
                                                                                                                               8 AA;
                                                                                                                                                                                                                                                         2 cfwkcty 8
                                                                                                                                                                                                                                 1 cywgcgy 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200011032-A2
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2000
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                                                                                                                                                                         Query Match
Best Local Si
Matches 4;
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                                                                                                                                                                                                                                                                                                                                                                AAY51899;
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   8886666666666
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Length 7;

51.5%; 80.0%;

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Query Match
Best Local Similarity
        7 A.A.;
                                                                                                                                                                                                                                                                 acromegaly
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                                                                                                                                                                                     AAW18456;
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                                                               Matches
                                                                                                                                                     AAW18456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somatostatin agonists include the somatostatin analogs shown in AARS6777 848 and AAR6074 83. These peptides are used in the invention to inhibit the accelerated growth of tumours. The growth is induced surgically and the tumour is of epithelial origin, eg. lung or colon tumours or partic. prostate or breast tumours, or melanoma. The peptides are known inhibitors of cancer cell growth and are partic. applied to the site of trauma, topically or subcutaneously.
                                                                                                                                                                 Gaps
         and selective pharmacological action than somatostatin. It has a structure inhibiting the activity of exopeptidases. It can be used in medicaments to inhibit tumour growth or the activity of tyrosine kinase enzymes involved in tumour growth ransformation. It is also useful
                                                   for regulating the release of growth hormone, insulin, glucagon and prolactin. It may also be used to inhibit pathological processes such as psoriasis, elicited by the pathological proliferation of
                                                                                                                                                                                                                                                                                                                                Somatostatin analog 41 - acts as agonist to inhibit tumour growth.
This peptide is a somatostatin analogue showing more advantageous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting accelerating tumour growth after trauma, esp surgery by treatment with somatostatin or its agonists, esp applied to the site of trauma
                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                    somatostatin; agonist; analog; accelerating tumour growth; t
surgery; treatment; solid primary tumour; metastatic tumour;
inhibition; tissue trauma; ulcer.
                                                                                                                                         Score 34; DB 13; Length 7; Pred. No. 6.4e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "H-Phe; D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 12; 33pp; English.
                                                                                                                                                                                                                                                                 AAR56817 standard; peptide; 7 AA.
                                                                                                                                          51.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US01412
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                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moreau J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-279685/34.
                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 4
                                                                                                          7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                         cywkc 6
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                                                                                    skin cells.
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                     AAR56817;
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                                                                                                                                           Query Match
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide(s) - which inhibit the release of for the treatment and diagnosis of tumours
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth hormone; tumour; Antarelix; Lanreotide; endocrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "L-2-methyltryptophan amide"
Score 34; DB 15;
Pred. No. 6.4e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Somatostatin analogue heptapeptide
                                                                                                                                                                                                                                                                                                                               AAW18456 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 15; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= OTHER
/note= "L-2-me
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New somatostatin analogue growth hormone, used e.g.
                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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2 cywkc 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a somatostatin agonist, that can be used in the method of the invention. The method is for the inhibition of fibrosis by the administration of somatostatin or particularly its agonists. The method is specifically used against fibrosis in the kidney, lung, liver or skin (particularly where caused by chemotherapy but also the result of glomerulonephritis, diabetes, cirrhosis, allograft rejection or infection with human immune deficiency virus), also in the central nervous system (e.g. intraocular fibrosis) or nose (e.g. masal polyposis). The method can be used therapeutically or prophylactically.
                                                                                                                                                                                                                                                                               Somatostatin; agonist; inhibitor; fibrosis; kidney; lung; liver; skin; chemotherapy; glomerulonephritis; diabetes; cirrhosis; nasal polyposis; allograft rejection; infection; human immune deficiency virus; therapy; central nervous system; intraocular fibrosis.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting fibrosis by administration of somatostatin or its agonists – particularly in lung, liver, kidney and skin, or where caused by chemotherapy
                                              ;
              Score 34; DB 18; Length 7; 
Pred. No. 6.4e+05; 
0; Mismatches 1; Indels
                                           0; Mismatches
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                                                                                                                                                                  AAY22068 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                             "note= "H-D-Phe"
                51.5%;
80.0%;
                                                                                                                                                                                                                                                      Somatostatin agonist peptide.
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Query Match
Best Local Similarity 80.vv,
4; Conservative
                                                                                                                                                                                                                            (first entry)
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Modified-site
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                                                                      1 cywgc 5
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|2 cywkc 6
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                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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Gaps

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Score 34; DB 19; Length 7; Pred. No. 6.4e+05; 0; Mismatches 1; Indels

51.5%; 80.0%;

4; Conservative

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Query Match Best Local Similarity Matches 4; Conserv

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Sequence 128, App
Sequence 128, App
Sequence 919, App
Sequence 919, App
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1, 
                                                                                                                                                                                                                                          August 12, 2002, 17:14:59 ; Search time 20.43 Seconds (without alignments) 9.565 Million cell updates/sec
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Sequence 10,
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/Pacyfiles1.pep:*
(cgn2_6/ptodata/2/iaa/backfiles1.pep:*
(cgn2_6/ptodata/2/iaa/backfiles2.pep:*
(cgn
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-488-659A-128
US-09-3082-298-919
US-09-3082-988-8
US-08-282-988-8
US-08-911-095-5
US-09-484-318-1
US-09-484-319-8
US-09-484-319-8
US-09-484-321-1
US-09-484-321-1
US-09-484-321-1
US-09-484-321-1
US-09-484-321-1
US-09-484-321-1
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US-09-484-321-1
US-09-484-321-1
US-09-484-321-1
US-09-355-769-1
US-09-355-769-1
US-09-355-769-1
US-09-356-670A-14
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     protein search, using sw model
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Sequence 5, Appliance 5, Appliance 1, Appliance 12, Appliance 12, Appliance 110, Appliance 11, Appli
                     Sequence 10, Appl
Sequence 10, Appl
Sequence 139, App
Sequence 139, App
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Sequence 6, Appli
Sequence 11, Appl
Sequence 29, Appl
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COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: O/J-UN-1995
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REEFERNCE/POCKET UNMBER: 31,815
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION FOR SO ID NO: 128:
SEQUENCE CHARACTERISTICS:
TENGTH: A mino acids
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US-09-195-726-10
US-09-067-755-10
US-08-487-006-139
US-08-488-659A-139
US-09-329-350-8
US-09-329-350-8
US-08-520-535-12
US-08-520-535-12
US-08-9142-110
US-08-41442-11
US-08-418-12519020-17
5506208-18
US-08-408-120-6
US-08-408-120-6
US-08-408-120-6
US-08-408-120-6
US-08-408-120-6
US-08-408-120-6
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US-08-487-006-128
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TOPOLOGY: linear
          \begin{array}{c} \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{g} \, \mathbf{
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US-08-487-006-128
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserva
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APPLICANT: Barney, 3
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US-09-315-304B-919
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US-08-282-980B-8
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                                       Gaps
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                                    0; Indels
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 Length 7;
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the C-terminal."
                                                                                                  RESULT 2
US-08-488-659A-128
Sequence 128, Application US/08488659A
Fatent No. 5919877
GENERAL INFORMATION:
APPLICANT: DOOLSY, Colette T.
APPLICANT: HOUGHTEN, Richard A.
TITLE OF INVENTION: Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES:
ADDRESSE: Campbell and Flores
STREET: A370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,659A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
Score 28; DB 1; 1
Pred. No. 1.7e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1705
RELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-082-279B-919
; Sequence 919, Application US/09082279B
 42.4%;
75.0%;
                                       Conservative
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OTHER INFORMATION:
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) OTHER INFORMATION:

US-08-488-659A-128
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TOPOLOGY: linear
Ouery Match
Best Local Similarity
Matches 3; Conserv
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| APPLICANT: GITTLE, KRIJY
| APPLICANT: GITTLE, KRIJY
| APPLICANT: GITTLE, KRIJY
| APPLICANT: GITTLE, GENERAL GENERAL APPLICANT: GITTLE, GENERAL WENTER, GENERAL APPLICANT: GITTLE, GENERAL WENTER, GENERAL BOOKERTIES
| ATTLE GE INVESTION UNDERS: 125/09/082.7798
| TITLE GE INVESTION UNDERS: 125/09/082.7798
| GITTLE GENERAL INFORMATION UNDERS: 125/09/082.7798
| GITTLE
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NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
OTHER INFORMATION: are linked by a covalent bond; the amino terminus
OTHER INFORMATION: is substituted with a methyl group."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: 1..3

COTHER INFORMATION: /label= Variant residues
COTHER INFORMATION: /note= "The Trp is in the D conformation."
US-08-931-095-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08286748B
Patent No. 5759542
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE DELIVERY
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson
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Query Match

40.9%; Score 27; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                      CALF: 00000
CALF: 00000
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,095
FLING DATE: 15-SEP-1997
CLASSIFICATION: 424
ATONNEY/AGENT INFORMATION:
NAME: NO. 6017512nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-OO
TELECOMMUNICATION INFORMATION:
TELEBRAX: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                            COUNTRY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-08-286-748B-7
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OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and carboxyl terminus
OTHER INFORMATION: are linked by a covalent bond."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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) OTHER INFORMATION: /label= Variant residues
) OTHER INFORMATION: /note= "The Trp is in the D conformation"
US-08-282-980B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08931095
; Patent No. 6017512
; GENERAL INFORMATION:
    APPLICANT: Dean, Richard T.
    APPLICANT: Lister-James, John
    TITLE OF INVENTION: Radiolabeled Peptides
    NUMBER OF SEQUENCES: 26
    CORRESPONDENCE ADDRESS:
    ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
    STREET: 300 South Wacker Drive, 32nd Floor
               APPLICANT: Dean, Richard T.
APPLICANT: Dean, Richard T.
APPLICANT: McBride, William
APPLICANT: Lister-James, John
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMCDONNell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,980B
FILING DATE: 29-UUL-1994
CLASSIFCATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No.592180an, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-1
TELECOMMUNTATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site LOCATION: 1..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circular
GENERAL INFORMATION:
                                                                                                                                                                                                                     Chicago
                                                                                                                                                                                                                                                                            USA
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CITY: Chicago
                                                                                                                                                                                                                                                                       COUNTRY: U
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US-08-931-095-5
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Gaps

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OTHER INFORMATION: Description of Artificial Sequence:Octreotide NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.9%; Score 27; DB 4; Length 8; 100.0%; Pred. No. 1.7e+05; Pred. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORDATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajaqopalan, Raghavan
APPLICANT: Bugaj, Joseph E.
APPLICANT: Bugaj, Joseph E.
TILLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
FILLE REFERENCE: DNA STRING
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEOFTWARE: Patentin Ver. 2.1
LENGTH: 8
                                                                                                                                     ; Sequence B. Application US/09484318; Patent No. 6180085; GENERAL INFORMATION: APPLICANT: AAchilefu, Samuel APPLICANT: Rajagopalan, Raghavan APPLICANT: Bugai, Joseph E. APPLICANT: Bugai, Joseph E.; TITLE OF INVENTION: NOVEL DYES FILE REFERENCE: DNA STRING CURRENT APPLICATION NUMBER: US/09/484,318; CURRENT FILING DATE: 2000-01-18; NUMBER OF SEO ID NOS: 8

SOFTHARE: Patentin Ver. 2.1
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OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
LOCATION: (2)..(7)
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; COCATION: (4); OTHER INFORMATION: This is D-tryptophan US-09-484-318-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09484319 Patent No. 6180086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 3; Conservative
1 cyw 3
| | | |
2 CYW 4
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                                                                                                           RESULT 9
US-09-484-318-8
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LENGTH: 8
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OTHER INFORMATION: Description of Artificial Sequence:Octreotide
NAME/KEY: SITE
OTHER INFORMATION: (1)
OTHER INFORMATION: This is D-phenylalanine
NAME/KEY: DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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LOCATION: (8)
OTHER INFORMATION: This C-terminal residue ends with a hydroxyl
US-09-484-318-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.9%; Score 27; DB 1; Length 8; 100.0%; Pred. No. 1.7e+05; ive 0; Mismatches 0; Indels
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40.9%; Score 27; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1.7e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa is D- -Naphthylalanine US-08-286-748B-7
                                                                                                                                                 NAME: J. PETER FASSE
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELEPHONE: (617) 542-5070
TELEPRX: (617) 542-8906
TELERX: (617) 542-8906
TELERX: (517) 542-8906
TELEX: (517) 542-8906
TELEX: (517) 542-8906
TELEX: SPOURACE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NOVEL DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,318
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO.1
LENGTH: 8
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NAME/KFY: SITE
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan
      APPLICATION NUMBER: US/08/286,748B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09484318 Patent No. 6180085
                        FILING DATE: August 5, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.9
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Gaps

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Sequence 8, Application US/09484320;
Sequence 8, Application US/09484320;
Sequence 8, Application US/09484320;
GENERAL INFORMATION:
APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: dnastrng
CURRENT APPLICATION UNDBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 8
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                       LENGTH: 8

LENGTH: 8

LENGTH: 8

ORGANISM: Artificial Sequence

FEATURE: OF STE

LOCATION: 10

OTHER INFORMATION: This is D-phenylalanine

LOCATION: (2)

LOCATION: (2)

LOCATION: (2)

LOCATION: (3)

LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
FEATURE:
FOATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: This is D-phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
40.9%; Score 27; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan NAME/KEY: SITE
LOCATION: (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: This is D-tryptophan US-09-484-320-8
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US-09-484-321-1
; Sequence 1, Application US/09484321
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (2)..(7)
NAME/KEY: SITE
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          SEQ ID NO 1
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APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Borshow, Richard B
APPLICANT: Borshow, Tunable Indocyanine Dyes For Biomedical Applications
ITILE REFERENCE: dnastrng
CURRENT APPLICATION NUMBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
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                                                          COTHER INFORMATION: This C-terminal residue ends with a hydroxyl US-09-484-319-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                              h 40.9%; Score 27; DB 4; Length 8; Similarity 100.0%; Pred. No. 1.7e+05; 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.9%; Score 27; DB 4; Length 8; 100.0%; Pred. No. 1.7e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Achilefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,319
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: This is D-phenylalanine MAME/KEY: DISULEID LOCATION: (2)..(7)
NAME/KEY: SITE.
LOCATION: (4)
OTHER INFORMATION: This is D-tryptophan NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , LUCATION: (4); OTHER INFORMATION: This is D-tryptophan US-09-484-319-8
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09484319
Patent No. 6180086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09484320 Patent No. 6180087
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ORGANISM: Artificial Sequence
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

RESULT

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18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
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                                    AAY03714 standard; peptide; 8 AA.
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/note= "D-form residue; optionally acetylated"

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                                                                                                                                                                                                     Radiolabeling thiol-containing peptides with fluorine-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-terminal acetylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "D-form residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fluorine-18 (F-18) labeled peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY03716 standard; peptide; 8 AA.
                                                                                                                                                                                                                                            Claim 13; Page 15; 22pp; English.
                 98WO-US18268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                         (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                    WPI; 1999-228967/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18F radionuclide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                 03-SEP-1998;
                                                                                                                              Griffiths GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY03716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :5
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The invention relates to a method for incorporating 18F radionuclide into peptide-containing targeting vectors for use in clinical positron emission temporaphy. Radiolabeling thiol-containing peptides with comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CR1R2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon across at least one leaving group comprising 1, Br. Cl. azide, tosylate, mesylate, nesylate, nesylate, ne m = 0-2; n+m = 0-2; x = 1, Br. Cl. azide, tosylate, mesylate, nosylate, rifilate, H, R2 = 1, Br. Cl. azide, tosylate, mesylate, nosylate, triflate, H, CONH2, COCH, OH, sulfonia caid, tertiary amine, quaternary ammonium, alkyl coptionally substituted by CONH2, COCH, OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl corquaternary ammonium, alkyl coptionally substituted by CONH2, COCH, OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl coptionally substituted by CONH2, COCH, OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl coptions as used for Radiolabeling peptide-containing creceptor-targeted peptides for was intibodies antibody fragments and receptor-targeted peptides for use in routine clinical positron emission tomography. The method is simple and efficient. The method uses the unique property of the free thiol groups which are rapidly alkylated at neutral pH and moderate temperature. Sequences AAY0374-716 represent examples of F-18 labeled peptides used in the method of detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Radiolabeling thiol-containing peptides with fluorine-18
"D-form residue; D-iodo-Tyr'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 20;
100.0%; Pred. No. 6.4e+05;
iive 0; Mismatches 0;
                                                                               /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY76816 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 15; 22pp; English.
                                                                                                                                                                                                                                                                                                                                       98WO-US18268
                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0057485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMUNOMEDICS INC.
    'note=
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Best Local Similarity
Matches 8; Conserv
                                            Misc-difference 8
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Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bi-specific antibodies that bind specific target tissue and targeted
                           Immunogenic peptide for bi-specific antibody recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                             Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-160561/14.
                                                                                                                                                                                                                                                     Misc-difference 8
                                                                                                                                                                             Misc-difference 3
                                                                                                                                                                                                     Misc-difference 5
                                                                                                                                                                                                                              Misc-difference 7
                                                                                                                                                    Misc-difference
                                                                                                                            Modified-site
     28-APR-2000
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                                                                                                                                                                                                                                                                                                                                         22-JUN-1999;
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14-OCT-1998;
                                                                                                                                                                                                                                                                                                                29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conjugates
                                                                                         Synthetic
   conjugate that is capable of carrying at least I diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targeted to methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable
                                                                                                                                 /note= "D-form residue; modified with free amino acid
group, protected amino acid group, chelating
agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                                                                                                                                                     Bi-specific antibodies that bind specific target tissue and targeted
                                 __note= "free amino acid group, protected amino acid
group, chelating agent or a metal-chelate
complex"
                                                                                                                                                                                                                                                                                                                                                                           Leung S, McBride WJ,
                                                                                    "D-form residue"
                                                                                                                                                                                   /note= "D-form residue"
                                                                                                                                                                                                            /note= "D-form residue"
                                                                                                           note= "D-form residue"
           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                        98US-0104156.
                                                                                                                                                                                                                                                                                     99WO-US13879
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                                                                                                                                                                                                                                                                                                                                                                       Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                 (IMMU-) IMMUNOMEDICS INC.
                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-160561/14
                                                                     Misc-difference 3
                                                                                                                                                                      Misc-difference 8
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                    Misc-difference
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                                                                                                                                                                                                                                                                                                                        14-OCT-1998;
                                                                                                                                                                                                                                                             29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                       Hansen HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                      conjugates
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Leung S, McBride WJ,

'note= "acetylated D-form residue"

'note= "D-form iodo-Tyr"

/note= "D-form residue"

99WO-US13879

'note= "D-form iodo-Tyr"

Location/Qualifiers /note= "acetylated"

(first entry)

'note= "D-form residue"

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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating a bi-specific diseased tissues in a patient comprishing administering a bi-specifically antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo
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Claim 23; Page 61; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 87.5 tes 7; Conservative
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Matches
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Gaps

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Length 9; Indels

100.0%; Score 59; DB 21; 100.0%; Pred. No. 6.4e+05; ive 0; Mismatches 0;

8; Conservative

1 gywgkgyw 8 

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Best Local Similarity

Matches

Query Match

RESULT AAB18511

AAY76818 standard; peptide; 8 AA.

AAY76818

AAY76818
ID AAY70
XX
AC AAY70
XX

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27-JUL-2000; 2000WO-CA00883
         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1365 AA;
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                                                                                                                                                                 N-PSDB; AAQ38899
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                                                                       05-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2001.
                             US5194600-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2001
                                                  16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast KRE5
                                                                                                                                    Boone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB72446;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a H2 homologue of a prolyl tripoptidase (designated DPP) from Porphyromonas gingivalis. The prolyl tripoptidase has an amidolytic activity, and cleaves a peptide bond in a target polypeptide having at least 4 amino acids. This bond is between a proline and an amino acid attached to the alpha-carboxyl group end of the proline. The polypeptide is useful for identifying inhibitors. These inhibitors are then useful for reducing the growth of bacterium or for protecting an animal from a periodontal disease such as ginglytics and periodontilis caused by
                                                                                                                                                                                                                                                                                                             Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful for identifying its inhibitor which is useful for protecting an animal from a periodontal disease such as gingivitis and periodontitis
                                                                                  Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast; cell wall; beta-glucan; assembly; pathway; KRE1; KRE5; growth; secretory; O-linked mannose; (1>6)-beta-glucan; epistasis; morphology; hydrophilic; glycoprotein; COOH-terminal; endoplasmic reticulum; ER; retention signal; antifungal agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 21; Length 841;
Pred. No. 54;
0; Mismatches 1; Indels
                                                             12 homologue of prolyl-tripeptidyl peptidase DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR36780 standard; Protein; 1365 AA.
AAB18511 standard; protein; 841 AA
                                                                                                                                                                                                                      UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                        Travis J, Potempa J, Banbula A;
                                                                                                                                                                                                                                                                                                                                                        Claim 22; Fig 6; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.4%;
85.7%;
                                                                                                                                                                            03-MAR-2000; 2000WO-US05551
                                                                                                                                                                                                99US-0123148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                        (first entry)
                                                                                           gingivitis; periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas gingivalis.
                                                                                                                Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                            WPI; 2000-594181/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                (TRAV/) TRAVIS J.
(POTE/) POTEMPA J.
(BANB/) BANBULA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 ywgsgyw 725
                                                                                                                                    WO200052147-A2.
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                                                                                                                                                                                                 05-MAR-1999;
                                        15-JAN-2001
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                                                                                                                                                         38-SEP-2000
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                    AAB18511;
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The sequences given in AAR34785 and AAR36780 represent proteins which participate in a yeast cell wall beta-glucan assembly pathway.

These proteins represent KREI and KRES respectively, and are essential for normal cell growth. KREI is a Ser/Thr rich protein probably probably probably probably through addition of O-linked mannose highly modified, probably through addition of O-linked mannose cesidues. Gene disruption of the KREI locus leads to a 40% reduced cesidues. Gene disruption of person of ABBS also caused defects in cell wall (1>6)-beta-glucan. Mutations at KRES also caused defects in cell wall (1>6)-beta-glucan production and appears to be defects in cell wall (1>6)-beta-glucan production and appears to be objected in which contains the COOH-terminal endoplasmic reticulum (ER) recention signal (His-Asp-Glu-Leu). Deletion of the KRES gene results in cells with aberant morphology and extremly compromised growth.

KREI and KRES are useful as tools for the in vitro screening of antifugal agents which inhibit fungi pathogenic to plants and animals.

The genes can be used to produce mutants for in vivo screening of antifungal agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding genes which participate in beta-glucan assembly - useful for producing mutants for in-vivo screening of antifungal agents and providing tools for in-vitro screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 1.2e+02;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                Sommer SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                        (ROYA-) ROYAL INST ADVANCEMENT LEARNING.
                                                                                                                                                                                                                                Meaden P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Columns 38-44; 24pp; English,
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                                                                                                                                                                                                                            Hill K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%;
75.0%;
90US-0488316
                                                                                90US-0488316
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Best Local Similarity 75.0°
'...a 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                Bussey H,
                                                                                                                                                                                                                                                                                                            WPI; 1993-109384/13.
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into peptide-containing targeting vectors for use in clinical position into peptide-containing targeting vectors for use in clinical position comparably. Radiolabeling thiol-containing peptides with fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F-(CH2)m-CRIRZ-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bears at least one leaving group comprising I, Br. CL, azide, tosylate, mosylate, nosylate, nosylate, in m = 0-2; n+m = 0-2; n
                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for incorporating 18F radionuclide
                                                                                                                                                                                                                                                                    Radiolabeling thiol-containing peptides with fluorine-18
                                                                                                                                                                                                                                                                                                       Claim 14; Page 15; 22pp; English.
                                                                 98WO-US18268.
                                                                                                                                                (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                            WPI; 1999-228967/19.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ywgkgyw 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            умдсдум 8
                                                                                                                                                                                      Griffiths GL;
                                                                 03-SEP-1998;
                                                                                                        03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-2000
                           11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY76817;
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ID AAY7
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          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                             The present invention relates to a method for determining the effect of a activity. The method comprises exposing an acceptor substrate for UGGT of a labelled donor in the presence of the test sample and UGGT. The method substrate for UGGT to is useful in glucosyltransferase assay and kinetics measurement for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for determining UGGT activity. UGGT is a soluble enzyme of the endoplasmic reticulum which catalyses the addition of a glucose residue onto reticulum clined oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence was used in a sequence homology comparison with rat UGGT (see AAF60732 and AAB72436) which was used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                         Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
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or protected thiol group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "D-form residue; optionally has a free or protected thiol group"
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Pred. No. 1.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                  Bergeron JJM, Thomas DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fluorine-18 (F-18) labeled peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                            Disclosure; Fig 9; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY03715 standard; peptide; 8 AA.
                                                        (CANA ) NAT RES COUNCIL CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.7%;
75.0%;
                  99us-0376330.
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Best Local Similarity 75.۰
امات 6
                                                                                              Tessier DC, Dignard D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
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                                                                                                                                                                                                                                      the presence of UGGT
                                                                                                                                    WPI; 2001-218358/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1234 gywkegyw 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 8
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                  18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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AAY03715
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protected amino acid group, chelating agent or a
metal-chelate complex"
                                                                                                                                                                                                                                           Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                         Gaps
                         ó
Length 8;
                                                                                                                                                                                                                   Immunogenic peptide for bi-specific antibody recognition.
                         1; Indels
76.3%; Score 45; DB 20;
85.7%; Pred. No. 6.4e+05;
            Pred. No. 6.4e+05;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                        AAY76817 standard; peptide; 8 AA.
                                                                                                                                                                                           (first entry)
                      Conservative
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Homo sapiens.
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30-JUN-2000;
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30-AUG-2000;
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06-SEP-2000;
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26-JUL-2000;
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14-AUG-2000;
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18-AUG-2000;
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                                                                                                                                                                                   24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
                                                                                                                        02-AUG-2001
        This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiarthritic; antirheumatic;
cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                 /note= "D-form residue; modified with free amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                           group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                                                                                                          Bi-specific antibodies that bind specific target tissue and targeted
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                                                                                                                                                                                                                                                  McBride WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human novel secreted protein, Seq ID 1230.
/note= "D-form residue"
Misc-difference 3
                                                                                                              /note= "D-form residue"
                            'note= "D-form residue"
                                                                                         'note= "D-form residue"
                                                                                                                                                                                                                                                  Leung S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU16277 standard; Protein; 164 AA.
                                                                                                                                                                                                                                                                                                                        Claim 22; Page 61; 76pp; English.
                                                                                                                                                                           99WO-US13879
                                                                                                                                                                                              98US-0090142
98US-0104156
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                                                                                                                                                                                                                                                  Hansen HJ, Griffiths GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                            (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                                                                                                                      WPI; 2000-160561/14
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Best Local Similarity
                                                                               Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
                                       Misc-difference
                                                                                                   Misc-difference
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                                                                                                                                   W09966951-A2
                                                                                                                                                                          22-JUN-1999;
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vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzhelmer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0225266.
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2000US-0231243.
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-SEP-2000; 2000US-0233064.

14-SEP-2000; 2000US-0233065.

21-SEP-2000; 2000US-0234305.

25-SEP-2000; 2000US-0234991.

25-SEP-2000; 2000US-0234991.

26-SEP-2000; 2000US-0235834.

27-SEP-2000; 2000US-0235834.

29-SEP-2000; 2000US-0235836.

29-SEP-2000; 2000US-0236369.

29-SEP-2000; 2000US-0236369.

29-SEP-2000; 2000US-0236369.

29-SEP-2000; 2000US-0236369.

29-SEP-2000; 2000US-0236369.

29-SEP-2000; 2000US-0236369.

20-OCT-2000; 2000US-0236399.

20-OCT-2000; 2000US-0236369.

20-OCT-2000; 2000US-0236369.

20-OCT-2000; 2000US-0234180.

20-OCT-2000; 2000US-024178.

20-OCT-2000; 2000US-024677.

20-OCT-2000; 2000US-0246611.

20-OCT-2000; 2000US-0246528.

20-OCT-2000; 2000
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2000US-0249297.
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2000US-0251868.
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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05-DEC-2000;
05-DEC-2000;
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17-NOV-2000;
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08-DEC-2000;
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or annellorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthitis.

Confidous autoimmune diseases e.g. rheumatoid arthitis of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other of and sounders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other of and wound healing and epithelial cell proliferation, to be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, antiarthritic, cardiant, monoclonal antibody; keloid, arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID No 1230; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB99111 standard; Protein; 152 AA.
                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0254099.
05-JAN-2001; 2001US-0254097.
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                                                                                                                                                                                                                                                                                           Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488783/53.
N-PSDB; AAS26264.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 ghwgkgew 132
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to grytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y
Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.6%; Score 44; DB 22; Length 10
75.0%; Pred. No. 2.5e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #19161.
                                                                                                                                                              useful in diagnosis and gene therapy
                                                                                                                                                                                                    Claim 20; Page 420; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG19170 standard; Protein; 1180 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                               WPI; 2001-476283/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
  Liu C, D
Wang D,
Yang Y, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1090 AA;
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                                                                                                    N-PSDB; AAK53220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2000;
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    Tang YT,
Zhao QA,
                                           Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, atherosclerosis, atopy, keloid and arthritis. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                           Human monoclonal antibodies recognizing human TGF-beta II receptor, useful for treating TGF-beta associated diseases such as tissue fibrosis.
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Pred. No. 38;
0; Mismatches 2; Indels
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2000US-0560875.
2000US-0598075.
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01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
                                           18-NOV-1999; 99JP-0328681.
08-NOV-2000; 2000JP-0340216.
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    17-NOV-2000; 2000WO-JP08129
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                                                                                                        (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                             Kamada M;
                                                                                                                                                                                   WPI; 2001-343825/36.
N-PSDB; AAH41153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
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01-SEP-2000;
15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2000;
20-JUN-2000;
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                                                                                                                                             Sakamoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                     fibrosis
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Gaps

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Length 1090;

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sequences of anti-adipocyte monoconal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver farugs of trougs directly to the far mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells. By complement mediated lysis. The antibodies may be labeled with a clear complement mediated lysis. The antibodies may be labeled with a used in methods of diagnosis in human subjects e.g. to determine the presence of adipocytes of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for observing the types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
                         AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 35820; 21pp. + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                71.2%; Score 42; DB 22; Length 121; 71.4%; Pred. No. 59; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 35820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB69676 standard; Protein; 126 AA.
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity
نکمح 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                          121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ywgkgyw 8
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                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymersae chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abernant protein expression or biological activity.
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                                                                                                                                                                                                                                                                                         The polypeptide and polynucieotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity
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Pred. No. 2.7e+02;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-adipocyte monoclonal antibody heavy chain, FAT 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                Claim 20; SEQ ID No 49529; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU02601 standard; Protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2000; 2000WO-GB03900.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-282031/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence . 1180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Gaps

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Claim 1; Page 156; 182pp; English.

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CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA consequences (ABL01840-ABL16175) and the encoded proteins consequence data for this patent did not form part of the printed consequence data for this patent did not format directly from WIPO cc specification, but was obtained in electronic format directly from WIPO cc at ftp.wipo.int/pub/published_pct_sequences.

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Query Match

Query Match

Alt.%; Score 42; DB 22; Length 126;
Best Local Similarity 71.4%; Pred. No. 61;
Best Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Aywnsgyw 43

Search completed: August 12, 2002, 17:21:41
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